

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: November 1, 2000, 10:25:11 ; Search time 3006.14 Seconds

(without alignments)
31.963 Million cell updates/sec

Title: us-09-202-455-6

Perfect score: 22

Sequence: 1 aagcccaagtcgtcgcac 22

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1033670 seqs, 2183789903 residues

Minimum number of hits satisfying chosen parameters: 2067340

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl:*

1: gb_bal:*
2: gb_ba2:*
3: gb_om:*
4: gb_ov:*
5: gb_pat:*
6: gb_ph:*
7: gb_pl1:*
8: gb_pl2:*
9: gb_pr1:*
10: gb_pr2:*
11: gb_pr3:*
12: gb_ro:*
13: gb_sy:*
14: gb_un:*
15: em_fun:*
16: em_hum1:*
17: em_hum2:*
18: em_in:*
19: em_om:*
20: em_or:*
21: em_ov:*
22: em_pat:*
23: em_ph:*
24: em_pl:*
25: em_ro:*
26: em_sy:*
27: em_sts:*
28: em_un:*
29: em_vl:*
30: gb_htg1:*
31: gb_htg2:*
32: gb_in1:*
33: gb_in2:*
34: em_ba1:*
35: em_ba2:*
36: em_hum3:*
37: em_hum4:*
38: gb_pr4:*
39: gb_htg3:*
40: gb_htg4:*
41: gb_htg5:*
42: gb_htg6:*
43: gb_htg7:*

44: em_htg1:*
45: em_htg2:*
46: em_htg3:*
47: em_hum5:*
48: gb_pl3:*
49: gb_pr5:*
50: gb_htg8:*
51: gb_htg9:*
52: gb_htg10:*
53: gb_htg11:*
54: gb_htg12:*
55: gb_htg13:*
56: gb_htg14:*
57: gb_in3:*
58: gb_htg15:*
59: gb_htg16:*
60: gb_htg17:*
61: em_htg4:*
62: em_htg5:*
63: em_htg6:*
64: em_htg7:*
65: em_hum6:*
66: gb_htg18:*
67: gb_htg19:*
68: gb_htg20:*
69: gb_htg21:*
70: gb_htg22:*
71: gb_htg23:*
72: gb_vl1:*
73: gb_vl2:*
74: gb_ba3:*
75: em_htg8:*
76: em_htg9:*
77: em_htg10:*
78: em_htg11:*
79: em_htg12:*
80: em_htg13:*
81: em_htg14:*
82: em_htg15:*
83: em_htg16:*
84: em_htg17:*
85: em_htg18:*
86: em_htg19:*
87: em_htg20:*
88: em_htg21:*
89: em_htg22:*
90: em_htg23:*
91: gb_pr6:*
92: gb_pr7:*
93: gb_sts1:*
94: gb_sts2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Length	ID	Description
C 1	22	100.0	754	12 AB032772	AB032772 Mus muscu
C 2	22	100.0	864	12 AB032771	AB032771 Mus muscu
C 3	22	100.0	951	12 AB008426	AB008426 Mus muscu
C 4	22	100.0	951	12 AB036798	AB036798 Mus muscu
C 5	22	100.0	2029	12 AB022036S4	AB022039 Mus muscu
C 6	22	100.0	2225	12 AF019048	AF019048 Mus muscu
C 7	22	100.0	2237	12 AF013170	AF013170 Mus muscu
C 8	22	100.0	2295	5 AR062119	AR062119 Sequence
C 9	22	100.0	2299	12 AF053713	AF053713 Mus muscu
C 10	18.8	85.5	930	9 AB037599	AB037599 Homo sapi
C 11	18.8	85.5	1823	11 AF013171	AF013171 Homo sapi
C 12	18.8	85.5	2201	11 AF019047	AF019047 Homo sapi

13 18.8 85.5 2271 11 AF053712
14 18.8 85.5 113451 52 AC023297
15 18.8 85.5 205139 66 AL139382
16 17.2 78.2 3747 74 VTBGLNTR
17 17.2 78.2 147481 58 AC067762
18 17.2 78.2 160952 56 AC055711
19 17.2 78.2 169853 59 AC069241
20 17.2 78.2 169331 59 AC069430
21 17.2 78.2 183957 52 AC024224
22 17.2 78.2 209137 30 AC06510
23 17.2 78.2 230254 60 AC074163
24 17.2 78.2 247029 40 AC006514
25 16.8 76.4 39739 31 AC015123
26 16.8 76.4 251796 69 AL358788
27 16.8 76.4 300732 32 AE003450
28 16.4 74.5 15301 48 SPB609
29 16.4 74.5 41037 42 AC017476
30 16.4 74.5 262131 32 AE003573
31 16.2 73.6 142 4 AF175474
32 16.2 73.6 142 4 AF175483
33 16.2 73.6 142 4 AF175484
34 16.2 73.6 142 4 AF175485
35 16.2 73.6 142 4 AF175487
36 16.2 73.6 142 4 AF175488
37 16.2 73.6 142 4 AF175489
38 16.2 73.6 142 4 AF175490
39 16.2 73.6 142 4 AF175492
40 16.2 73.6 143 4 AF175486
41 16.2 73.6 1058 12 AF053454
42 16.2 73.6 1086 1 AF013513
43 16.2 73.6 4269 91 AC017655
44 16.2 73.6 4729 91 HSATP1AX1
45 16.2 73.6 5618 92 HOMATP1G04

ALIGNMENTS

RESULT 1
LOCUS AB032772/C
DEFINITION Mus musculus RANKL 3 mRNA for receptor activator of NF-kB ligand 3, complete cds.
ACCESSION AB032772.1 GI:8843824
VERSION AB032772.1
KEYWORDS receptor activator of NF-kB ligand 3.
SOURCE Mus musculus CDNA to mRNA.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 Ikeda, T., Takahashi, H. and Hirokawa, K.
TITLE Somatostatin, a new marker of osteoblast, regulates the expression of RANKL isoforms
JOURNAL Unpublished (1999)
AUTHORS 2 (bases 754)
TITLE Ikeda, T.
JOURNAL Direct Submission
AUTHORS Submitted (28-SEP-1999) to the DDBJ/EMBL/GenBank databases. Tohru Ikeda, School of Medicine, Tokyo Medical and Dental University, Department of Pathology and Immunology, 1-5-45 Yushima, Bunkyo-ku, Tokyo 113-8519, Japan (E-mail: tohru.ph2med.tmd.ac.jp, Tel:81-3-5803-5176, Fax:81-3-5803-0123)
FEATURES
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1. 754
/organism="Mus musculus"
/db_xref="taxon:10090"
155. 754
/gene="RANKL 3"
155. 754
/gene="RANKL 3"
/codon_start=1
/product="receptor activator of NF-kB ligand 3"

/protein_id="BA097258.1"
/db_xref="GI:8843825"
/translation="MKQAFQGVKQELHIVGPOFSGAPAMWESWLDVNRGKPEA
QPFALHITNMAISIPSGSHKTYLTSWYDRGRKAKISNMTLISGKLRVNDGTYITANI
CFRHETSGSVPTDYLDLMTYVVTSTIKIPSSHLMGSGSTKNSGSEHFYSINVG
GFFKLRAGEEISIVSNPSLDDPDQDITYGAFKVDID"
BASE COUNT 209 a 190 c 185 g 170 t
ORIGIN
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Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 aagcccaaaagtaagtcgcatc 22
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Db 731 AAGCCCAAAAGTACGTCGCATC 710
RESULT 2
LOCUS AB032771/C
DEFINITION Mus musculus RANKL 2 mRNA for receptor activator of NF-kB ligand 2, complete cds.
ACCESSION AB032771.1 GI:8843822
VERSION AB032771.1
KEYWORDS receptor activator of NF-kB ligand 2.
SOURCE Mus musculus CDNA to mRNA.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 864)
AUTHORS Ikeda, T.
TITLE Receptor activator of NF-kB ligand 2
JOURNAL Published Only in Database (2000) In press
AUTHORS 2 (bases 1 to 864)
TITLE Ikeda, T.
JOURNAL Direct Submission
AUTHORS Submitted (28-SEP-1999) to the DDBJ/EMBL/GenBank databases. Tohru Ikeda, School of Medicine, Tokyo Medical and Dental University, Department of Pathology and Immunology, 1-5-45 Yushima, Bunkyo-ku, Tokyo 113-8519, Japan (E-mail: tohru.ph2med.tmd.ac.jp, Tel:81-3-5803-5176, Fax:81-3-5803-0123)
FEATURES
source
1. 864
/organism="Mus musculus"
/db_xref="taxon:10090"
1. 864
/gene="RANKL 2"
1. 864
/gene="RANKL 2"
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/product="receptor activator of NF-kB ligand 2"
/protein_id="BA097257.1"
/db_xref="GI:8843823"
/translation="MRRASRDYGVLTPTPMSFLLALGLGVOVCSIALFLYFRA
QMDPNRISDSSTHCFFYRLRLHVNAGLQDSTLEEDLPPGCRMKQAFQGVKPEA
HIVGPOFSGAPAMWESWLDVNRGKAKISNMTLISGKLRVNDGTYITANI
CFRHETSGSVPTDYLDLMTYVVTSTIKIPSSHLMGSGSTKNSGSEHFYSINVG
GFFKLRAGEEISIVSNPSLDDPDQDITYGAFKVDID"
BASE COUNT 221 a 227 c 219 g 197 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 aagcccaaaagtaagtcgcatc 22
|||||
Db 841 AAGCCCAAAAGTACGTCGCATC 820

RESULT 3
AB008426/c 951 bp mRNA ROD 02-MAY-1998
LOCUS Mus musculus mRNA for osteoclast differentiation factor (ODF),
DEFINITION complete cds.
ACCESSION AB008426
VERSION AB008426.1 GI:3041781
KEYWORDS osteoclast differentiation factor (ODF).
SOURCE Mus musculus bone marrow stromal cells cell_line:ST2 CDNA to mRNA,
clone_11b:pcDL-SRA296 clone:POBM291.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 951)
AUTHORS Yasuda, H.
TITLE Direct Submission
JOURNAL Submitted (22-OCT-1997) to the DDBJ/EMBL/GenBank databases.
Hinatake Yasuda, Snow Brand Milk Products Co., Ltd., Research
Institute of Life Science, 519 Shimo-Tsibashi, Ishidashi-machi,
Tochigi 329-05, Japan (E-mail: fvpd7042emb.infoweb.or.jp,
Tel:0285-52-1331, Fax:0285-53-1314)
2 (sites)
REFERENCE 2 (sites)
AUTHORS Yasuda, H., Shima, N., Nakagawa, N., Yamaguchi, K., Kinoshita, M.,
Mochizuki, S., Tomoyasu, A., Yano, K., Goto, M., Murakami, A., Tsuda, E.,
Moriwaga, T., Higashio, K., Udagawa, N., Takahashi, N. and Suda, T.
TITLE Osteoclast differentiation factor is a ligand for
osteoprotegerin/osteoclastogenesis-inhibitory factor and is
identical to TRANCE/RANKL
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3597-3602 (1998)
MEDLINE 98188248
FEATURES
SOURCE
Location/Qualifiers
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/organism="Mus musculus"
/db_xref="taxon:10090"
/cell_line="ST2"
/cell_type="stromal cells"
/clone="POBM291"
/clone_11b="pcDL-SRA296"
/tissue_type="bone marrow"
1..951
/codon_start=1
/product="osteoclast differentiation factor (ODF)"
/protein_id="BA025425.1"
/db_xref="GI:3041782"
/translation="MRRASRDYKYLRSSEMGSGPGVPHGPIHPAPAPAPPA
ASRSMFLALGLIGVYCSIALFLYRAQMDPRISDSHCTRLRLRHENGLD
STLESEDTLPSCRRMKAQAFQAVOKELQHTVQRRSGAPAMEGSLDVAQGRKE
AOPFAHLITNAASIPSGSHKVTLSWHDGMAKISMTLSNGKLRVNOGFYLLVAN
ICFRHETSGSVPTDYQLMAYVYKTSIKIPSSHMLMGSGSTKMWGNSSEHFYSIN
GGFFKLRAGEISIOVSNPDLDPDQATYGAFAKVGQID"
misc_feature 142..213
/note="transmembrane domain"
misc_feature 454..948
/note="Tumor Necrosis Factor (TNF)-like domain"
BASE COUNT 231 a 267 c 248 g 205 t
ORIGIN

Query Match 100.0%; Score 22; DB 12; Length 951;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 aagcccaaatgacgtcgatc 22
|||||
DB 928 AAGCCCAAAAGTACGTCGCATC 907

RESULT 4
LOCUS AB036798/c 951 bp mRNA ROD 29-JUN-2000
DEFINITION Mus musculus mRNA for RANKL 1, complete cds.
ACCESSION AB036798

VERSION AB036798.1 GI:8843829
KEYWORDS RANKL 1.
SOURCE Mus musculus cDNA to mRNA.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 951)
AUTHORS Ikeda, T.
TITLE Published Only in Database (2000) In press
JOURNAL RANKL 1
REFERENCE 2 (bases 1 to 951)
AUTHORS Ikeda, T.,
TITLE Direct Submission
JOURNAL Submitted (11-JUN-2000) to the DDBJ/EMBL/GenBank databases. Tohru
Ikeda, School of Medicine, Tokyo Medical and Dental University,
Department of Pathology and Immunology, 1-5-45 Yushima, Bunkyo-ku,
Tokyo 113-8519, Japan (E-mail: toru.pth@med.tmd.ac.jp,
Tel:81-3-5803-5176, Fax:81-3-5803-0123)
FEATURES
SOURCE
Location/Qualifiers
1..951
/organism="Mus musculus"
/db_xref="taxon:10090"
1..951
/note="receptor activator of nuclear factor kappa B
ligand"
1
/codon_start=1
/product="RANKL 1"
/protein_id="BA07259.1"
/db_xref="GI:8843830"
/translation="MRRASRDYKYLRSSEMGSGPGVPHGPIHPAPAPAPPA
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STLESEDTLPSCRRMKAQAFQAVOKELQHTVQRRSGAPAMEGSLDVAQGRKE
AOPFAHLITNAASIPSGSHKVTLSWHDGMAKISMTLSNGKLRVNOGFYLLVAN
ICFRHETSGSVPTDYQLMAYVYKTSIKIPSSHMLMGSGSTKMWGNSSEHFYSIN
GGFFKLRAGEISIOVSNPDLDPDQATYGAFAKVGQID"
BASE COUNT 231 a 267 c 248 g 205 t
ORIGIN

Query Match 100.0%; Score 22; DB 12; Length 951;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 aagcccaaatgacgtcgatc 22
|||||
DB 928 AAGCCCAAAAGTACGTCGCATC 907

RESULT 5
LOCUS AB022036S4/c 2029 bp DNA ROD 14-APR-2000
DEFINITION Mus musculus DNA for osteoclast differentiation factor, exon 5,
complete cds.
ACCESSION AB022036
VERSION AB022036.1 GI:4127268
KEYWORDS osteoclast differentiation factor.
SEGMENT 4 of 4
SOURCE Mus musculus (strain:129) embryonic stem cell DNA.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (sites)
AUTHORS Kodaira, K., Kodaira, K., Mizuno, A., Yasuda, H., Shima, N.,
Murakami, A., Ueda, M. and Higashio, K.
TITLE Cloning and characterization of the gene encoding mouse osteoclast
differentiation factor
JOURNAL Gene 230 (1), 121-127 (1999)
MEDLINE 99214075
REFERENCE 2 (bases 1 to 2029)
AUTHORS Kodaira, K.
TITLE Direct Submission
JOURNAL Submitted (05-JAN-1999) to the DDBJ/EMBL/GenBank databases.
Kunihiko Kodaira, YS New Technology Institute Inc., Molecular

Biology: Shimomishashi 519, Ishibashi-machi, Tochigi 329-0512,
Japan (E-mail:YENITEF-cnet.or.jp, Tel:81-285-52-2821,
Fax:81-285-52-2824)

FEATURES

SOURCE

Location/Qualifiers

1..2029 /organism="Mus musculus"

/strain="129" /db_xref="taxon:10090"

CDS

/cell_type="embryonic stem cell"
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AB022038.1:146..182,AB022038.1:274..372,159..580)

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/codon_start=1 /protein_id="BA36970.1"

/db_xref="GI:4127270"

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STLESDTLDPSCRRMKAQFQAVQKELHIVGPQRTSAMEGSWLDVADQKPEADP
FAHJLTINAASIPSGSHKVTLSWYHDKGMATISMTLSNGKLRYNODGFYLYANICF
RHETSGSVPTDYQLMWYVYKTSIKIPSSHNLKMGSTKNWGSNSEFHFYSINVGAF
FKLRAGEISTIOVSNPILDDPDQATYFGAFKYQDID"

exon

159..1043

/number=5 /product="osteoclast differentiation factor"

BASE COUNT 620 a 334 c 412 g 663 t

ORIGIN

Query Match 100.0%; Score 22; DB 12; Length 2029;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 aagcccaagtagctgcac 22
|||||
Db 557 AAGCCCAAGTACGTGCATC 536

RESULT 6

AF019048/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

JOURNAL

FEATURES

SOURCE

TITLE

JOURNAL

MEDLINE

JOURNAL

FEATURES

SOURCE

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FEATURES

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FEATURES

SOURCE

TITLE

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MEDLINE

JOURNAL

FEATURES

SOURCE

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/product="RANKL"
/protein_id="BAB86812.1"
/db_xref="GI:2612924"

BASE COUNT

623 a 468 c 523 g 611 t

ORIGIN

Query Match 100.0%; Score 22; DB 12; Length 2225;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 aagcccaagtagctgcac 22
|||||

Db 1064 AAGCCCAAGTACGTGCATC 1043

RESULT 7

AF013170/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

JOURNAL

FEATURES

SOURCE

TITLE

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CDS

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/cell_line="T cell hybridoma KMs-8.3.5"
142..1092
/note="TNF-related ligand"
/codon_start=1
/product="TRANCE"
/protein_id="AAC71061.1"
/db_xref="GI:2411498"
/translation="MRRASRDYGYKLRSESGSGPGVPHGEPHLPAPASAPAPPA
ASRSMFLALIGLGOVCSIALFLYFRAOMDPRISDSSTCEFRILRLHENAIGLOD
STLSEEDLPDSCRRMROFQAVOKEOHAYGPRFSGARPMAGSMIDVAKRKE
AOPFAHLTINASTPSGSHKVTLSWYHDROAKTSNMTLSNGKLRVNDGFFYYAN
ICFRHETSGSPYDYLQMYVYVTSIKIPSHNLMKGGSTKMWGSGNSERHFYSIN
GGFKLRAGEEISIVSNPSLDPDQATYFGAFKVDID"

BASE COUNT 636 a 470 c 519 g 612 t

ORIGIN

Query Match

Best Local Similarity 100.0%; Score 22; DB 12; Length 2237;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 aagccccaagctgcgcgc 22
|||||
Db 1069 AAGCCCAAGTACGTCGATC 1048

RESULT 8

AR062119 2295 bp DNA PAT 29-SEP-1999
LOCUS AR062119/c
DEFINITION Sequence 6 from patent US 5843678.
ACCESSION AR062119
VERSION AR062119.1 GI:5989810
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2295)
AUTHORS Boyle,W.J.
TITLE Osteoprotegerin binding proteins
JOURNAL Patent: US 5843678-A 6 01-DEC-1998;
FEATURES
source 1..2295
location/Qualifiers
BASE COUNT 648 a 487 c 538 g 622 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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|||||
Db 1085 AAGCCCAAGTACGTCGATC 1064

RESULT 9
AF053713 2299 bp mRNA ROD 09-MAY-1998
LOCUS AF053713/c
DEFINITION Mus musculus osteoprotegerin ligand mRNA, complete cds.
ACCESSION AF053713
VERSION AF053713.1 GI:3057147
KEYWORDS
SOURCE house mouse.
ORGANISM Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 2299)
Lacey,D.L., Timms,E., Tan,H.-L., Kelley,M.J., Dunstan,C.R.,
Burgess,T., Elliott,R., Colombero,A., Elliott,G., Scully,S.,
Hsu,H., Sullivan,J., Hawkins,N., Davy,E., Capparelli,C., Eli,A.,
Qian,Y.-X., Kaufman,S., Sarosi,I., Shalhoub,V., Senaldi,G., Guo,J.,

TITLE Delaney,J. and Boyle,W.J.
JOURNAL Osteoprotegerin ligand is a cytokine that regulates osteoclast
differentiation and activation
MEDLINE Cell 93 (2), 165-176 (1998)
REFERENCE 98227661
AUTHORS 2 (bases 1 to 2299)
TITLE Boyle,W.J.
JOURNAL Direct Submission

Submitted (16-MAR-1998) Department of Cell Biology, Amgen, Inc.,
One Amgen Center Drive, Thousand Oaks, California 91320, USA

FEATURES
source 1..2299
location/Qualifiers
1..2299
/organism="Mus musculus"
/db_xref="taxon:10090"
170..1120
/function="regulates osteoclast differentiation and
activation"
/codon_start=1
/product="osteoprotegerin ligand"
/protein_id="AAC40113.1"
/db_xref="GI:3057148"

CDS

BASE COUNT 641 a 494 c 541 g 623 t
ORIGIN

Query Match 100.0%; Score 22; DB 12; Length 2299;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 aagccccaagctgcgcgc 22
|||||
Db 1097 AAGCCCAAGTACGTCGATC 1076

RESULT 10
AB037599 930 bp mRNA PRI 06-APR-2000
LOCUS AB037599/c
DEFINITION Homo sapiens mRNA for SODF/TRANCE, complete cds.
ACCESSION AB037599
VERSION AB037599.1 GI:6863047
KEYWORDS sodf/trance; SODF/TRANCE.
SOURCE Homo sapiens male tongue epithelial-like squamous cell carcinoma
cell_line:SCC-4 CDNA to mRNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1 (sites)
Nagai,M., Kyakumoto,S. and Sato,N.
Cancer cells responsible for humoral hypercalcemia express mRNA
encoding a secreted form of ODF/TRANCE that induces osteoclast
formation

JOURNAL Biochem. Biophys. Res. Commun. 269 (2), 532-536 (2000)
MEDLINE 20175237
AUTHORS Nagai,M., Kyakumoto,S. and Sato,N.
TITLE Direct Submission
JOURNAL Submitted (26-JAN-2000) to the DDBJ/EMBL/Genbank databases.
Masazumi Nagai, Iwate Medical University School of Dentistry,
Department of Biochemistry, 19-1 Uchiyama, Morioka, Iwate 020-8505,
Japan (E-mail:imagai@iwate-med.ac.jp, Tel: +81-19-651-5111 (ex.436),
Fax: +81-19-654-4147)

FEATURES

source 1..930
location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="SCC-4"
/cell_type="epithelial-like squamous cell carcinoma"

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          PSGSHKVSLSWYHDHNGAKISMTFTSNGKLIYNODGFYLLANICFRHHTSGDLAT
          EYLQIMVYVTKTSIKIPSSHLMKGGSTKYMSGNSEPHFYSINVGGFRLRSGEISL
          EVSNPSLIDPDODATYFGAFKVRDID"

BASE COUNT      283 a      184 c      200 g      260 t      3 others
ORIGIN
      85.5%; Score 18.8; DB 9; Length 930;
      90.9%; Pred. No. 12;
      0; Mismatches 2; Indels 0; Gaps 0;
      20; Conservative 0;

Query Match
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      |||||
      20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
      20; Conservative 0;

Db      806 AACCCCAAGTATGTCATC 785

RESULT 11
AF013171 1823 bp mRNA PRI 19-SEP-1997
LOCUS Homo sapiens TNF-related ligand TRANCE mRNA, partial cds.
DEFINITION AF013171
ACCESSION AF013171
VERSION AF013171.1 GI:2411499
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1823)
Wong,B.R., Rho,J., Arron,J., Robinson,E., Orlicky,J., Chao,M.,
Kalachikov,S., Cayani,E., Bartlett,F.S. III, Frankel,W.N., Lee,S.Y.
and Choi,Y.
TRANCE is a novel ligand of the tumor necrosis factor receptor
family that activates c-Jun N-terminal kinase in T cells
J. Biol. Chem. 272 (40), 25190-25194 (1997)
JOURNAL MEDLINE
REFERENCE 2 (bases 1 to 1823)
Wong,B.R., Rho,J., Arron,J., Lee,S.Y., Robinson,E. and Choi,Y.
Direct Submission
Submitted (09-JUL-1997) Howard Hughes Medical Institute, The
Rockefeller University, 1230 York Ave., New York, NY 10021, USA
JOURNAL
FEATURES
source
1..1823
Location/Qualifiers
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/db_xref="taxon:9606"
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1..738
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/product="TRANCE"
/protein_id="AAC51762.1"
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/translation="OMDPNRISDGHGHCYIRILRLHENDFODTTLIESODTKLIPDSR
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EYLQIMVYVTKTSIKIPSSHLMKGGSTKYMSGNSEPHFYSINVGGFRLRSGEISL
EVSNPSLIDPDODATYFGAFKVRDID"

BASE COUNT      569 a      305 c      380 g      569 t

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ORIGIN
Query Match
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      90.9%; Pred. No. 12;
      0; Mismatches 2; Indels 0; Gaps 0;
      20; Conservative 0;

Query Match
      1 aagccccaagtcgcgcac 22
      |||||
      20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
      20; Conservative 0;

Db      715 AACCCCAAGTATGTCATC 694

RESULT 12
AF019047 2201 bp mRNA PRI 22-NOV-1997
LOCUS Homo sapiens receptor activator of nuclear factor kappa B ligand
DEFINITION AF019047
ACCESSION AF019047
VERSION AF019047.1 GI:2612921
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 2201)
Anderson,D.M., Maraskovsky,E., Billingsley,W.L., Dougall,W.C.,
Tometsko,M.E., Roux,E.R., Teepe,M.C., Dubose,R.F., Cosman,D. and
Galibert,L.
A homologue of the TNF receptor and its ligand enhance T-cell
growth and dendritic-cell function
Nature 390 (6656), 175-179 (1997)
JOURNAL MEDLINE
REFERENCE 2 (bases 1 to 2201)
Anderson,D.M., Billingsley,W., Dougall,W., Maraskovsky,E.,
Cosman,D., Dubose,R. and Galibert,L.
Direct Submission
Submitted (13-AUG-1997) Molecular Biology, Immunex Corp., 51
University St., Seattle, WA 98101, USA
JOURNAL
FEATURES
source
1..2201
Location/Qualifiers
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EAQPFPAHLITINADIPSGSHKVSLSWYHDHNGAKISMTFTSNGKLIYNODGFYLLA
NICFRHHTSGDLAT EYLQIMVYVTKTSIKIPSSHLMKGGSTKYMSGNSEPHFYSIN
VGGFRLRSGEISL EVSNPSLIDPDODATYFGAFKVRDID"

BASE COUNT      658 a      429 c      497 g      617 t
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Query Match
      85.5%; Score 18.8; DB 11; Length 2201;
      90.9%; Pred. No. 12;
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      20; Conservative 0;

Query Match
      1 aagccccaagtcgcgcac 22
      |||||
      20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
      20; Conservative 0;

Db      1059 AACCCCAAGTATGTCATC 1038

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RESULT 13
AF053712/c 2271 bp mRNA PRI 09-MAY-1998
LOCUS Homo sapiens osteoprotegerin ligand mRNA, complete cds.
ACCESSION AF053712
VERSION AF053712.1 GI:3057145
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS 1 (bases 1 to 2271)
Lacey, D.L., Timms, E., Tan, H.-L., Kelley, M.J., Dunstan, C.R.,
Burgess, T., Elliott, R., Colombero, A., Elliott, G., Scully, S.,
Hsu, H., Sullivan, J., Hawkins, N., Davy, E., Capparelli, C., Eli, A.,
Qian, Y.-X., Kaufman, S., Sarosi, I., Shalhoub, V., Senaldi, G., Guo, J.,
Delaney, J. and Boyle, W.J.
Osteoprotegerin ligand is a cytokine that regulates osteoclast
differentiation and activation
Cell 93 (2), 165-176 (1998)
MEDLINE 98227661
JOURNAL 2 (bases 1 to 2271)
REFERENCE Boyle, W.J.
AUTHORS Direct Submission
JOURNAL Submitted (16-MAR-1998) Department of Cell Biology, Amgen, Inc.,
One Amgen Center Drive, Thousand Oaks, California 91320, USA
FEATURES
SOURCE
CDS
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/db_xref="taxon:9606"
185..1138
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/product="osteoprotegerin ligand"
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TLESODFTLIPDSGRRIQAFQAGAVQKELQHVQSHIRAEKAMVDGSLDLAKSKL
EAPQPAHLINTDIPSGSHKYSLSWYHDMGAKISMTFNGKLIYNODFFYLYA
NICRHHHTSGDLATEYLOIMWYVTKSIKIPSSHTLMKSGTKWKSNSSEHFFYSIN
VGGFRLKSGEISIEVSFSLDDPDQATYTGAKRVADIP"
BASE COUNT 658 a 462 c 522 g 629 t
ORIGIN

AUTHORS
Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,
Anderson, S., Baldwin, J., Barna, N., Beda, F., Boguslavsky, L.,
Boukhgalter, B., Brown, A., Burkett, G., Campopiano, A., Castle, A.,
Chapel, V., Colangelo, M., Collins, S., Collymore, A., Cooke, P.,
Deatellano, K., Dewar, K., Dodge, S., Domino, M., Doyle, M.,
Fenster, J., Ferreira, P., FitzHugh, W., Forrest, C., Gage, D.,
Galagan, J., Gargy, S., Ginde, S., Goyette, M., Graham, L.,
Grand-Pierre, N., Grant, G., Hagos, B., Heald, A., Horton, L.,
Howland, J., C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karas, A.,
Klein, J., Landers, T., Larcocque, K., Lehoczy, J., Levine, R.,
Lieu, C., Liu, G., Locke, K., MacDonald, P., Marquis, N., McCarthy, M.,
McEwan, P., McGurk, A., McKernan, K., McPheters, R., Meldrum, J.,
Menais, L., Mihov, T., Miranda, C., Mlenga, V., Morrow, J., Naylor, J.,
Norman, C., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, T., M.,
Peterson, K., Pierre, N., Pisan, C., Pollara, V., Raymond, C.,
Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S.,
Severy, P., Spencer, B., Stange, Thomas, N., Stojanovic, N.,
Subramanian, A., Talmas, J., Testayre, S., Theodore, J., Tirelli, A.,
Travers, M., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B.,
Wu, X., Wyman, D., Ye, W.-J., Young, G., Zainoun, J., Zimmer, A. and
Zody, M.
JOURNAL
TITLE
COMMENT
Direct Submission
Submitted (11-FEB-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Mar 3, 2000 this sequence version replaced gi:1139552.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIRB
Web site: http://www.seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: 14020
Center clone name: 21.H.9
----- Summary Statistics
Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 106493 bases at least Q40
Consensus quality: 109791 bases at least Q40
Consensus quality: 111178 bases at least Q20
Insert size: 138000; agarose-fp
Insert size: 112251; sum-of-contigs
Quality coverage: 3.5 in Q20 bases; agarose-fp
Quality coverage: 4.3 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 13 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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2255 2364: gap of 100 bp
2355 6779: contig of 4415 bp in length
6730 6879: gap of 100 bp
11333 11332: contig of 4433 bp in length
6830 11332: gap of 100 bp
11333 11332: contig of 4433 bp in length
11333 17335: contig of 5903 bp in length
17336 17435: gap of 100 bp
17436 23308: contig of 5873 bp in length
23309 23408: gap of 100 bp
23409 28598: contig of 5190 bp in length
28599 28698: gap of 100 bp
28699 36183: contig of 7485 bp in length
36134 36283: gap of 100 bp
36234 44529: contig of 8246 bp in length
44530 44629: gap of 100 bp
44630 53672: contig of 9043 bp in length

* 53673 53772: gap of 100 bp
* 53773 62948: contig of 9176 bp in length
* 62949 63048: gap of 100 bp
* 63049 75673: contig of 12625 bp in length
* 75674 75773: gap of 100 bp
* 75774 92375: contig of 16602 bp in length
* 92376 92475: gap of 100 bp
* 92476 113451: contig of 20976 bp in length.
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11433. 17335
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44630. 53672
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53773. 62948
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clone_end:SP6
vector_side:right"
63049. 75673
/note="assembly_fragment"
75774. 92375
/note="assembly_fragment"
92476. 113451
/note="assembly_fragment"
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Best Local Similarity 90.9%; Pred. No. 14;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 aagcccaagatcgatcgatc 22
DB 12283 AAGCCCAAGATCGATCGATC 12304
RESULT 15
AL139382 205139 bp DNA HTG 06-JUL-2000
LOCUS AL139382/C
DEFINITION Homo sapiens chromosome 13 clone RP11-86N24, *** SEQUENCING IN
PROGRESS ***, 27 unordered pieces.
ACCESSION AL139382
VERSION AL139382.4 GI:8978069
KEYWORDS HTG; HTGS_PHASE1.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 205139)
AUTHORS Burton,J.
TITLE Direct Submission
JOURNAL Submitted (05-JUL-2000) Sanger Centre, Hinxton, Cambridgeshire,

COMMENT

CB10 1SA: UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequests@sanger.ac.uk
On Jul 7, 2000 this sequence version replaced gi:8386479.

Genome Center
Center: Sanger Centre
Center code: SC
Web site: <http://www.sanger.ac.uk>
Contact: humquery@sanger.ac.uk

Project Information
Center project name: Ba86N24

Summary Statistics
Assembly program: XGAP4; version 4.5
Sequencing vector: Plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 193731 bases at least Q40
Consensus quality: 198268 bases at least Q20
Insert size: 202539; sum-of-contigs
Insert size: 162413; 9.2% error; agarose-1p
Quality coverage: 3.08x in Q20 bases; sum-of-contigs Quality coverage: 3.84x in Q20 bases; agarose-1p

* NOTE: This is a 'working draft' sequence. It currently consists of 27 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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* 19331 32371: contig of 13041 bp in length
* 32372 32471: gap of 100 bp
* 32472 34870: contig of 2399 bp in length
* 34871 34970: gap of 100 bp
* 34971 42014: contig of 7044 bp in length
* 42015 42114: gap of 100 bp
* 42115 50153: contig of 8039 bp in length
* 50154 50253: gap of 100 bp
* 50254 56692: contig of 6439 bp in length
* 56693 56792: gap of 100 bp
* 56793 61250: contig of 4458 bp in length
* 61251 61350: gap of 100 bp
* 61351 62561: contig of 1211 bp in length
* 62562 62661: gap of 100 bp
* 62662 75173: contig of 12512 bp in length
* 75174 75273: gap of 100 bp
* 75274 81438: contig of 6165 bp in length
* 81439 81538: gap of 100 bp
* 81539 87285: contig of 5747 bp in length
* 87286 87385: gap of 100 bp
* 87386 89590: contig of 2205 bp in length
* 89591 89690: gap of 100 bp
* 89691 91525: contig of 1835 bp in length
* 91526 91625: gap of 100 bp
* 91626 106940: contig of 15315 bp in length
* 106941 107040: gap of 100 bp
* 107041 115418: contig of 8378 bp in length
* 115419 115518: gap of 100 bp
* 115519 119162: contig of 3644 bp in length
* 119163 119262: gap of 100 bp
* 119263 121311: contig of 2049 bp in length
* 121312 121411: gap of 100 bp
* 121412 129170: contig of 7759 bp in length
* 129171 129270: gap of 100 bp
* 129271 141607: contig of 12337 bp in length
* 141608 141707: gap of 100 bp
* 141708 152435: contig of 10728 bp in length
* 152436 152535: gap of 100 bp
* 152536 158440: contig of 5905 bp in length
* 158441 158540: gap of 100 bp
* 158541 159553: contig of 1013 bp in length


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* 159554 159653: gap of 100 bp
* 159654 164333: contig of 4680 bp in length
* 164334 164433: gap of 100 bp
* 164434 182240: contig of 17807 bp in length
* 182241 182340: gap of 100 bp
* 182341 183761: contig of 1421 bp in length
* 183762 183861: gap of 100 bp in length
* 183862 188214: contig of 4353 bp in length
* 188215 188314: gap of 100 bp
* 188315 205139: contig of 16825 bp in length.
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    /clone_ID="RPC1-11.1"
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      clone_end:T7
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      19331. 32371
        /note="assembly_fragment:01284"
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      32472. 34870
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        fragment_chain:1"
      34971. 42014
        /note="assembly_fragment:00149"
        fragment_chain:1"
      42115. 50153
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      50254. 56692
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        fragment_chain:2"
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        /note="assembly_fragment:00612"
        fragment_chain:2"
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      81539. 87285
        /note="assembly_fragment:01144"
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      87386. 89590
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        /note="assembly_fragment:01146"
        fragment_chain:5"
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        /note="assembly_fragment:00498"
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Search completed: November 1, 2000, 14:52:32
 Job time: 16041 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OK nucleic - nucleic search, using sw model

Run on: November 1, 2000, 14:52:32 ; Search time 3006.14 Seconds
(without alignments)
29.058 Million cell updates/sec

Title: us-09-202-455-9

Perfect score: 20

Sequence: 1 atcagaagacagactact 20

Scoring table: IDENTITY_NDC
Gapop 10.0 , Gapext 1.0

Total number of hits satisfying chosen parameters: 2067340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl:*
1: gb_da1:*
2: gb_da2:*
3: gb_da3:*
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5: gb_da5:*
6: gb_da6:*
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11: gb_da11:*
12: gb_da12:*
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1	20	100.0	468	12 AB022036S2	AB022037 Mus muscu
2	20	100.0	754	12 AB032772	AB032772 Mus muscu
3	20	100.0	754	12 AB032771	AB032771 Mus muscu
4	20	100.0	864	12 AB008426	AB008426 Mus muscu
5	20	100.0	951	12 AB036798	AB036798 Mus muscu
6	20	100.0	2225	12 AF019048	AF019048 Mus muscu
7	20	100.0	2237	12 AF013170	AF013170 Mus muscu
8	20	100.0	2295	5 AR062119	AR062119 Sequence
9	20	100.0	2299	12 AF053713	AF053713 Mus muscu
10	18.4	92.0	66390	53 AC025129	AC025129 Homo sapi
11	18	90.0	182673	59 AC073105	AC073105 Homo sapi
12	18	90.0	186176	42 AC016994	AC016994 Homo sapi

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

c	13	18	90.0	189949	9	AC005040	Homo sapi
c	14	17.4	87.0	52	5	AR062114	Sequence
c	15	17.4	87.0	120515	91	HSJ744124	
c	16	17.4	87.0	133925	9	AC004562	AC004562 Homo sapi
c	17	17.4	87.0	151578	70	AP001074	AP001074 Homo sapi
c	18	17.4	87.0	170992	70	AP001786	AP001786 Homo sapi
c	19	17.4	87.0	172288	67	AL160164	AL160164 Homo sapi
c	20	17.4	87.0	174389	67	AL353598	AL353598 Homo sapi
c	21	17.4	87.0	175674	56	AC053465	AC053465 Homo sapi
c	22	17.4	87.0	176781	30	AC002989	AC002989 Homo sapi
c	23	17.4	87.0	177555	10	AC006450	AC006450 Homo sapi
c	24	17.4	87.0	179563	70	AP001521	AP001521 Homo sapi
c	25	17.4	87.0	179783	54	AC025988	AC025988 Homo sapi
c	26	17.4	87.0	193780	54	AC026004	AC026004 Homo sapi
c	27	17.4	87.0	225311	67	AL158052	AL158052 Homo sapi
c	28	17.4	87.0	323210	70	AP002397	AP002397 Homo sapi
c	29	17.4	87.0	332071	89	AP000905	AP000905 Homo sapi
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c	33	17	85.0	194899	53	AC025763	AC025763 Homo sapi
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c	37	16.8	84.0	2271	12	AF053712	AF053712 Homo sapi
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c	39	16.8	84.0	99295	68	AL356673	AL356673 Homo sapi
c	40	16.8	84.0	127272	69	AL357973	AL357973 Homo sapi
c	41	16.8	84.0	141954	68	AL355480	AL355480 Homo sapi
c	42	16.8	84.0	152210	51	AC022910	AC022910 Homo sapi
c	43	16.8	84.0	157848	43	AC018455	AC018455 Homo sapi
c	44	16.8	84.0	159472	51	AC022491	AC022491 Homo sapi
c	45	16.8	84.0	160342	53	AC025492	AC025492 Homo sapi

ALIGNMENTS

RESULT 1
AB02203652 468 bp DNA ROD 14-APR-2000
LOCUS Mus musculus DNA for osteoclast differentiation factor, exon 2.
ACCESSION AB022037
VERSION AB022037.1 GI:4127266
KEYWORDS osteoclast differentiation factor.
SEGMENT 2 of 4
SOURCE Mus musculus (strain:129) male embryonic stem cell cell_line:E14
DNA.

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
1 (sites)
Kodaira, K., Kodaira, K., Mizuno, A., Yasuda, H., Shima, N.,
Muraikami, A., Ueda, M. and Higashio, K.
Cloning and characterization of the gene encoding mouse osteoclast
differentiation factor
JOURNAL Gene 230 (1), 121-127 (1999)
MEDLINE 99214075
REFERENCE 2 (bases 1 to 468)
AUTHORS Kodaira, K.
TITLE Direct Submission
Submitted (05-JAN-1999) to the DDBJ/EMBL/GenBank databases.
Kunihiko Kodaira, YS New Technology Institute Inc., Molecular
Biology, Shimomishibashi 519, Ishibashi-machi, Tochigi 329-0512,
Japan (E-mail:YKNET-net.or.jp, Tel:81-285-52-2821,
Fax:81-285-52-2824)

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BASE COUNT 137 a 111 c 98 g 122 t

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Db 186 ATCAGAAGACGACTACT 205

RESULT 2
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LOCUS Mus musculus RANKL 3 mRNA for receptor activator of NF-kB ligand 3,
complete cds.
DEFINITION AB032772
ACCESSION AB032772
VERSION AB032772.1 GI:8843824
KEYWORDS receptor activator of NF-kB ligand 3.
SOURCE Mus musculus cDNA to mRNA.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
1 (sites)
Ikeda, T., Takahashi, H. and Hirokawa, K.
Somatostatin, a new marker of osteoblast, regulates the expression
of RANKL isoforms
JOURNAL Unpublished (1999)
REFERENCE 2 (bases 1 to 754)
AUTHORS Ikeda, T.
TITLE Direct Submission
Submitted (28-SEP-1999) to the DDBJ/EMBL/GenBank databases. Tohru
Ikeda, School of Medicine, Tokyo Medical and Dental University,
Department of Pathology and Immunology, 1-5-45 Yushima, Bunkyo-ku,
Tokyo 113-8519, Japan (E-mail:toru.phn2med.tmd.ac.jp,
Tel:81-3-5803-5176, Fax:81-3-5803-0123)

FEATURES

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BASE COUNT 231 a 267 c 248 g 205 t

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OY 1 atcagaagacgactcact 20
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DB 240 ATCAGAGACGACTACT 259

RESULT 6
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LOCUS Mus musculus receptor activator of nuclear factor kappa B ligand
DEFINITION (RANKL) mRNA, complete cds.
ACCESSION AF019048
VERSION AF019048.1 GI:2612923
KEYWORDS house mouse.
SOURCE Mus musculus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 2225)
Anderson, D.M., Maraskovsky, E., Billingsley, W.L., Dougall, W.C.,
Tometsko, M.E., Roux, E.R., Teepe, M.C., Dubose, R.F., Cosman, D. and
Gallbert, L.
A homologue of the TNF receptor and its ligand enhance T-cell
growth and dendritic-cell function
Nature 390 (6565), 175-179 (1997)
JOURNAL MEDLINE
REFERENCE 2 (bases 1 to 2225)
Anderson, D.M., Billingsley, W., Dougall, W., Maraskovsky, E.,
Cosman, D., Dubose, R. and Gallbert, L.
Direct Submission
Submitted (13-AUG-1997) Molecular Biology, Immunex Corp., 51
University St., Seattle, WA 98101, USA
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BASE COUNT 623 a 468 c 523 g 611 t

Query Match 100.0%; Score 20; DB 12; Length 2225;
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OY 1 atcagaagacgactcact 20
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DB 376 ATCAGAGACGACTACT 395

RESULT 7
AF013170 2237 bp mRNA ROD 05-NOV-1998
LOCUS Mus musculus TNF-related ligand TRANCE mRNA, complete cds.
DEFINITION AF013170
ACCESSION AF013170
VERSION AF013170.1 GI:2411497
KEYWORDS house mouse.
SOURCE Mus musculus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 2237)
Wong, B.R., Rho, J., Arron, J., Robinson, E., Orlinick, J., Chao, M.,
Kalachikov, S., Cayani, E., Bartlett, F.S. III, Frankel, W.N., Lee, S.Y.
and Choi, Y.
TRANCE is a novel ligand of the tumor necrosis factor receptor
family that activates c-Jun N-terminal kinase in T cells
J. Biol. Chem. 272 (40), 25190-25194 (1997)
J. Biol. Chem. 272 (40), 25190-25194 (1997)
2 (bases 1 to 2237)
Wong, B.R., Josten, R., Lee, S.Y., Sauter, B., Li, H.L., Steinman, R.M.
and Choi, Y.
TRANCE (tumor necrosis factor [TNF]-related activation-induced
cytokine), a new TNF family member predominantly expressed in T
cells, is a dendritic cell-specific survival factor
J. Exp. Med. 186 (12), 2075-2080 (1997)
J. Exp. Med. 186 (12), 2075-2080 (1997)
3 (bases 1 to 2237)
Fuller, K., Wong, B., Fox, S., Choi, Y. and Chambers, T.J.
TRANCE is necessary and sufficient for osteoclast-mediated
activation of bone resorption in osteoclasts
J. Exp. Med. 188 (5), 997-1001 (1998)
J. Exp. Med. 188 (5), 997-1001 (1998)
4 (bases 1 to 2237)
Wong, B.R., Josten, R., Lee, S.Y., Vologodskaya, M., Steinman, R.M. and
Choi, Y.
The TNF family of signal transducers mediates NF-kappaB activation
by the TRANCE receptor
J. Biol. Chem. 273 (43), 28355-28359 (1998)
J. Biol. Chem. 273 (43), 28355-28359 (1998)
5 (bases 1 to 2237)
Wong, B.R., Rho, J., Arron, J., Lee, S.Y., Robinson, E. and Choi, Y.
Direct Submission
Submitted (09-JUL-1997) Howard Hughes Medical Institute, The
Rockefeller University, 1230 York Ave., New York, NY 10021, USA
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 complete cds.
 AB032771
 ACCESSION AB032771.1 GI:8843822
 KEYWORDS receptor activator of NF-kB ligand 2.
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 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 864)
 AUTHORS Ikeda, T.
 TITLE Receptor activator of NF-kB ligand 2
 JOURNAL Published Only in Database (2000) In press
 REFERENCE 2 (bases 1 to 864)
 AUTHORS Ikeda, T.
 TITLE Direct Submission
 JOURNAL Submitted (28-SEP-1999) to the DDBJ/EMBL/GenBank databases. Tohru
 Ikeda, School of Medicine, Tokyo Medical and Dental University,
 Department of Pathology and Immunology, 1-5-45 Yushima, Bunkyo-ku,
 Tokyo 113-8519, Japan (E-mail: toru.pth2@med.tmd.ac.jp,
 Tel:81-3-5803-5176, Fax:81-3-5803-0123)
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 complete cds.
 ACCESSION AB008426
 VERSION AB008426.1 GI:3041781
 KEYWORDS osteoclast differentiation factor (ODF).
 SOURCE Mus musculus bone marrow stromal cells cell_line:ST2 CDNA to mRNA,
 clone.lib:pCDL-SRa296 clone:pOBM291.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
 Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 951)
 AUTHORS Yasuda, H.
 TITLE Direct Submission
 JOURNAL Submitted (22-OCT-1997) to the DDBJ/EMBL/GenBank databases.
 Hisataka Yasuda, Snow Brand Milk Products Co., Ltd., Research
 Institute of Life Science, 519 Shimo-Isihashi, Ishibashi-machi,
 Toohigi 329-05, Japan (E-mail: fvyd7042@mb.infoweb.or.jp,

REFERENCE 2 (sites)
 AUTHORS Yasuda, H., Shima, N., Nakagawa, N., Yamaguchi, K., Kinoshita, M.,
 Mochizuki, S., Tomoyasu, A., Yano, K., Goto, M., Murakami, A., Tsuda, E.,
 Morinaga, T., Higashio, K., Udagawa, N., Takahashi, N. and Suda, T.
 TITLE Osteoclast differentiation factor is a ligand for
 osteoprotegerin/osteoclastogenesis-inhibitory factor and is
 identical to TRANCE/RANKL
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3597-3602 (1998)
 MEDLINE 98188248
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 1 atcagaagacagcactcact 20
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 VERSION AB036798.1 GI:8843829
 KEYWORDS RANKL 1.
 SOURCE Mus musculus CDNA to mRNA.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 951)
 AUTHORS Ikeda, T.
 TITLE Direct Submission
 JOURNAL Submitted (11-JAN-2000) to the DDBJ/EMBL/GenBank databases. Tohru
 Ikeda, School of Medicine, Tokyo Medical and Dental University,
 Department of Pathology and Immunology, 1-5-45 Yushima, Bunkyo-ku,
 Tokyo 113-8519, Japan (E-mail: toru.pth2@med.tmd.ac.jp,
 Tel:81-3-5803-5176, Fax:81-3-5803-0123)
 FEATURES
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BASE COUNT 636 a 470 c 519 g 612 t

ORIGIN

Query Match 100.0%; Score 20; DB 12; Length 2237;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 atcagaagacgactact 20
|||||

Db 381 ATCAGAGACGACTACT 400

RESULT 8
AR062119 2295 bp DNA PAT 29-SEP-1999
SEQUENCE 6 from patent US 5843678.
ACCESSION AR062119
VERSION AR062119.1 GI:5989810
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 2295)
AUTHORS Boyle, W.J.
TITLE Osteoprotegerin binding proteins
JOURNAL Patent: US 5843678-A 6 01-DEC-1998;
FEATURES Location/Qualifiers
Source 1..2295

BASE COUNT 648 a 487 c 538 g 622 t
ORIGIN

Query Match 100.0%; Score 20; DB 5; Length 2295;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 atcagaagacgactact 20
|||||

Db 397 ATCAGAGACGACTACT 416

LOCUS AF053713 2299 bp mRNA ROD 09-MAY-1998
DEFINITION Mus musculus osteoprotegerin ligand mRNA, complete cds.
ACCESSION AF053713
VERSION AF053713.1 GI:3057147
KEYWORDS
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 2299)

REFERENCE Lacey, D.L., Timms, E., Tan, H.-L., Kelley, M.J., Dunstan, C.R.,
Burgess, T., Elliott, R., Colombero, A., Elliott, G., Scully, S.,
Hsu, H., Sullivan, J., Hawkins, N., Davy, E., Capparelli, C., Eli, A.,
Qian, Y.-X., Kaufman, S., Sasaki, I., Shalhoub, V., Senaldi, G., Guo, J.,
DeLaney, J., and Boyle, W.J.
TITLE Osteoprotegerin ligand is a cytokine that regulates osteoclast
differentiation and activation
JOURNAL Cell 93 (2), 165-176 (1998)
MEDLINE 98227661
REFERENCE 2 (bases 1 to 2299)
AUTHORS Boyle, W.J.
TITLE Direct Submission
JOURNAL Submitted (16-MAR-1998) Department of Cell Biology, Amgen, Inc.,
One Angen Center Drive, Thousand Oaks, California 91320, USA

FEATURES

SOURCE Location/Qualifiers
1..2299
/organism="Mus musculus"
/db_xref="taxon:10090"
CDS 170..1120
/function="regulates osteoclast differentiation and
activation"
/codon_start=1
/product="osteoprotegerin ligand"
/protein_id="AAC40113.1"
/db_xref="GI:3057148"

BASE COUNT 641 a 494 c 541 g 623 t
ORIGIN

Query Match 100.0%; Score 20; DB 12; Length 2299;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 atcagaagacgactact 20
|||||

Db 409 ATCAGAGACGACTACT 428

RESULT 10
AC025129 66390 bp DNA HTG 21-MAR-2000
LOCUS Homo sapiens clone RP11-362B23, WORKING DRAFT SEQUENCE, 8 unordered
DEFINITION pieces.
ACCESSION AC025129
VERSION AC025129.2 GI:7272258
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 66390)
REFERENCE Birren, B., Linton, L., Nusbaum, C. and Lander, E.
AUTHORS
TITLE Homo sapiens, clone RP11-362B23
JOURNAL Unpublished
AUTHORS 2 (bases 1 to 66390)
Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,
Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F.,
Boguslavsky, L., Bouhagalter, B., Brown, A., Burkett, G.,
Campoliano, A., Castle, A., Choe, A., Colangelo, M., Collins, S.,
Collumora, A., Cooke, P., Dearlano, K., Dewar, K., Diaz, J.S.,
Dodg, S., Domini, M., Doyle, M., Ferreira, P., FitzHugh, W., Gage, D.,
Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L.,
Grand, P., Grant, G., Hagos, B., Heatford, A., Horton, L.,
Howland, J., J. C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karakas, A.,
Klein, J., Labocque, K., Lamazares, R., Landers, T., Lehoczy, J.,
Levine, R., Liecu, G., Liu, G., Locke, K., MacDonald, P., Marquis, N.,
McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R.,
Meidrum, J., Menus, L., Minova, T., Miranda, C., Mlenka, V., Morrow, J.,
Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P.,
O'Neill, D., Oliver, T.M., Oliver, J., Peterson, K., Pierre, N.,
Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D.,
Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B.,
Stange-Tromann, N., Stojanovic, N., Subramanian, A., Talamas, J.,
Testave, S., Theodore, J., Tirrell, A., Travers, M., Trigglio, J.,
Vassiliou, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, R.,
Young, G., Zainoun, J., Zimmer, A. and Zody, M.

TITLE Direct Submission
JOURNAL Submitted (05-MAR-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT On Mar 21, 2000 this sequence version replaced g1:7158940.
All repeats were identified using RepeatMasker.

Smith, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: http://www.seq.wi.mit.edu

Contact: sequence_submissions@genome.wi.mit.edu

----- Project Information

Center project name: 17803

Center clone name: 362_B.23

----- Summary Statistics

Sequencing Vector: M13; M7815; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.960731

Consensus quality: 62647 bases at least Q40

Consensus quality: 64420 bases at least Q30

Consensus quality: 65095 bases at least Q20

Insert size: 55000; agarose-fp

Insert size: 65690; sum-of-ctrls

Quality coverage: 4.8 in Q20 bases; agarose-fp

Quality coverage: 4.0 in Q20 bases; sum-of-ctrls

* NOTE: This is a 'working draft' sequence. It currently
* consists of 8 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

* 1 1204: contig of 1204 bp in length
* 1205 1304: gap of 100 bp
* 1305 3155: contig of 1851 bp in length
* 3156 3255: gap of 100 bp
* 3256 6760: contig of 3505 bp in length
* 6761 6860: gap of 100 bp
* 6861 9249: contig of 2389 bp in length
* 9250 9349: gap of 100 bp
* 9350 18770: contig of 9421 bp in length
* 18771 18870: gap of 100 bp
* 18871 29847: contig of 10977 bp in length
* 29848 29947: gap of 100 bp
* 29948 47118: contig of 17171 bp in length
* 47119 47218: gap of 100 bp
* 47219 66390: contig of 19172 bp in length.

FEATURES

----- Location/Qualifiers

1..66390

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="RP11-362823"

/clone.lib="RPC1-11 Human Male BAC"

1..1204

/note="assembly-fragment"

1305..3155

/note="assembly-fragment"

3256..6760

/note="assembly-fragment"

6861..9249

/note="assembly-fragment"

clone_end:SP6

vector_side:left"

9350..18770

/note="assembly-fragment"

18871..29847

/note="assembly-fragment"

29948..47118

/note="assembly-fragment"

47219..66390

/note="assembly-fragment"

BASE COUNT 17609 a 14210 c 15018 g 18846 t 707 others
ORIGIN

Query Match 92.0%; Score 18.4; DB 53; Length 66390;
Best Local Similarity 95.0%; Pred. No. 11;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0

1 atcagaagacagcactcact 20

Db 7233 ATCAGAACGACGAACTACT 7252

RESULT 11

AC073105/c

LOCUS

DEFINITION

SEQUENCE, 28 unordered pieces.

ACCESSION

AC073105

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
----- Project Information -----
Center project name: H.NH0464P18
----- Summary Statistics -----
Sequencing vector: M13; 100%
Chemistry: Dye-terminator Big Dye; 100% of reads
Chemistry: Dye-terminator Big Dye; 0% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 168154 bases at least Q40
Consensus quality: 172308 bases at least Q30
Consensus quality: 174249 bases at least Q20
Insert size: 178000; agarose-fp
Insert size: 179973; sum-of-ctrls
Quality coverage: 3.67 in Q20 bases; agarose-fp
Quality coverage: 3.72 in Q20 bases; sum-of-ctrls

COMMENT

* NOTE: This is a 'working draft' sequence. It currently
* consists of 28 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

* 1 1558: contig of 1558 bp in length
* 1559 1658: gap of unknown length
* 1659 3238: contig of 1580 bp in length
* 3239 3338: gap of unknown length
* 3339 6471: contig of 3132 bp in length
* 6471 6570: gap of unknown length
* 6571 9019: contig of 2449 bp in length
* 9020 9119: gap of unknown length
* 9120 11319: contig of 2200 bp in length
* 11320 11419: gap of unknown length
* 11420 14077: contig of 2658 bp in length
* 14078 14177: gap of unknown length
* 14178 17503: contig of 3326 bp in length


```
* 17504 17603: gap of unknown length
* 17604 21392: contig of 3789 bp in length
* 21393 21492: gap of unknown length
* 21493 24939: contig of 3447 bp in length
* 24940 25039: gap of unknown length
* 25040 29068: contig of 4029 bp in length
* 29069 33082: gap of unknown length
* 29169 33083 33182: contig of 3914 bp in length
* 33083 33183 36815: gap of unknown length
* 36815 42224: contig of 3633 bp in length
* 36916 42225: gap of unknown length
* 42225 42324: contig of 5309 bp in length
* 42325 47877: gap of unknown length
* 47878 47978: contig of 5553 bp in length
* 47978 52325: gap of unknown length
* 52326 52425: contig of 4348 bp in length
* 52426 57081: gap of unknown length
* 57082 57181: contig of 4656 bp in length
* 57182 63081: gap of unknown length
* 63082 63181: contig of 5900 bp in length
* 63182 69925: gap of unknown length
* 69926 70025: contig of 6744 bp in length
* 70026 79877: gap of unknown length
* 79878 79978: contig of 9852 bp in length
* 79978 87549: gap of unknown length
* 87550 87650: contig of 7572 bp in length
* 87650 97089: gap of unknown length
* 97090 97189: contig of 9440 bp in length
* 97190 105647: gap of unknown length
* 105648 105748: contig of 8458 bp in length
* 105749 115419: gap of unknown length
* 115420 115519: gap of 9672 bp in length
* 115520 124377: gap of unknown length
* 124378 124478: contig of 8858 bp in length
* 124479 136660: gap of unknown length
* 136661 136761: contig of 12183 bp in length
* 136762 151613: gap of unknown length
* 151614 151713: gap of 14853 bp in length
* 151714 165051: contig of 13338 bp in length
* 165052 165152: gap of unknown length
* 165153 182673: contig of 17522 bp in length.
```

FEATURES

SOURCE

```
1. 182673
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="2"
/clone="Rp11-464P18"
misc_feature
1. 1558
/note="assembly_name:Contig4"
misc_feature
1659. 3238
/note="assembly_name:Contig5"
misc_feature
3339. 6470
/note="assembly_name:Contig6"
misc_feature
6571. 9019
/note="assembly_name:Contig7"
misc_feature
9120. 11319
/note="assembly_name:Contig8"
misc_feature
11420. 14077
/note="assembly_name:Contig9"
misc_feature
14178. 17503
/note="assembly_name:Contig10"
clone_end:"7"
vector_side:"left"
misc_feature
17604. 21392
/note="assembly_name:Contig11"
misc_feature
21493. 24939
/note="assembly_name:Contig12"
misc_feature
25040. 29068
/note="assembly_name:Contig13"
misc_feature
29169. 33082
/note="assembly_name:Contig14"
misc_feature
33183. 36815
```

```
/note="assembly_name:Contig15"
/clone_end:"SP6"
/vector_side:"right"
misc_feature
36916. 42224
/note="assembly_name:Contig16"
misc_feature
42325. 47877
/note="assembly_name:Contig17"
misc_feature
47978. 52325
/note="assembly_name:Contig18"
misc_feature
52426. 57081
/note="assembly_name:Contig19"
misc_feature
57182. 63081
/note="assembly_name:Contig20"
misc_feature
63182. 69925
/note="assembly_name:Contig21"
misc_feature
70026. 79877
/note="assembly_name:Contig22"
misc_feature
79978. 87549
/note="assembly_name:Contig23"
misc_feature
87650. 97089
/note="assembly_name:Contig24"
misc_feature
97190. 105647
/note="assembly_name:Contig25"
misc_feature
105748. 115419
/note="assembly_name:Contig26"
misc_feature
115520. 124377
/note="assembly_name:Contig27"
misc_feature
124478. 136660
/note="assembly_name:Contig28"
misc_feature
136761. 151613
/note="assembly_name:Contig29"
misc_feature
151714. 165051
/note="assembly_name:Contig30"
misc_feature
165152. 182673
/note="assembly_name:Contig31"
BASE COUNT 53616 a 35139 c 34992 g 56222 t 2704 others
ORIGIN
```

```
Query Match 90.0%; Score 18; DB 59; Length 182673;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 atcagaagacagcactca 18
|||||
DB 139699 ATCAGAGACAGCAGCTCA 139682
```

```
RESULT 12
AC016994 AC016994 186176 bp DNA HTG 16-JUL-2000
LOCUS Homo sapiens chromosome 2 clone RP11-19J8, WORKING DRAFT SEQUENCE,
DEFINITION 16 unordered pieces.
ACCESSION AC016994.5 GI:9230814
VERSION HTG: HTGS-PHASE1; HTGS-DRAFT.
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 186176)
AUTHORS Waterston,R.H.
TITLE The sequence of Homo sapiens clone
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 186176)
AUTHORS Waterston,R.H.
TITLE Direct Submission
JOURNAL Submitted (09-DEC-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
COMMENT On Jul 16, 2000 this sequence version replaced gi:8569724.
----- Genome Center -----
```

```

Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
----- Project Information -----
Center project name: H_NH0015J08
----- Summary Statistics -----
Sequencing vector: M13, 71%
Sequencing vector: plasmid; 29%
Chemistry: Dye-primer ET; 71% of reads
Chemistry: Dye-terminator Big Dye; 29% of reads
Assembly program: Phrap; version 0.990315
Consensus quality: 177898 bases at least Q40
Consensus quality: 180830 bases at least Q30
Consensus quality: 182405 bases at least Q20
Insert size: 187000; agarose-fp
Insert size: 184676; sum-of-contigs
Quality coverage: 6.89 in Q20 bases; agarose-fp
Quality coverage: 6.04 in Q20 bases; sum-of-contigs
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 16 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1 1389: contig of 1389 bp in length
* 1390 1489: gap of unknown length
* 1490 2756: contig of 1267 bp in length
* 2757 2856: gap of unknown length
* 2857 4074: contig of 1218 bp in length
* 4075 4174: gap of unknown length
* 4175 5443: contig of 1269 bp in length
* 5444 5543: gap of unknown length
* 5544 6701: contig of 1158 bp in length
* 6702 6801: gap of unknown length
* 6802 8009: contig of 1208 bp in length
* 8010 8109: gap of unknown length
* 8110 9195: contig of 1086 bp in length
* 9196 9295: gap of unknown length
* 9296 10487: contig of 1192 bp in length
* 10488 10587: gap of unknown length
* 10588 12117: contig of 1530 bp in length
* 12118 12217: gap of unknown length
* 12218 13331: contig of 1114 bp in length
* 13332 13431: gap of unknown length
* 13432 15095: contig of 1664 bp in length
* 15096 15195: gap of unknown length
* 15196 17531: contig of 2336 bp in length
* 17532 17632: gap of unknown length
* 17632 20593: contig of 2964 bp in length
* 20596 20695: gap of unknown length
* 20696 39643: contig of 18948 bp in length
* 39644 39743: gap of unknown length
* 39744 86154: contig of 46411 bp in length
* 86155 86254: gap of unknown length
* 86255 186176: contig of 99922 bp in length.
*
* Location/Qualifiers
* 1. 186176
* /organism="Homo sapiens"
* /db_xref="taxon:9606"
* /chromosome="2"
* /clone="RP11-19J8"
* 1. 13389
* /note="assembly_name:Contig11"
* 1490. 2756
* /note="assembly_name:Contig22"
* 2857. 4074
* /note="assembly_name:Contig27"
* 4175. 5443
* /note="assembly_name:Contig28"
* 5544. 6701

```

```

misc_feature      /note="assembly_name:Contig29"  
                  .6802..8009  
                  /note="assembly_name:Contig30"  
                  .8110..9195  
misc_feature      /note="assembly_name:Contig31"  
                  .9296..10487  
misc_feature      /note="assembly_name:Contig32"  
                  .10588..12117  
misc_feature      /note="assembly_name:Contig33"  
                  .12218..13331  
misc_feature      /note="assembly_name:Contig35"  
                  .13432..15095  
misc_feature      /note="assembly_name:Contig37"  
                  .15196..17531  
misc_feature      /note="assembly_name:Contig38"  
                  .17632..20595  
misc_feature      /note="assembly_name:Contig39"  
                  .20696..39643  
                  /note="assembly_name:Contig40  
                  clone_end:SP6  
                  vector_side:right"  
                  .39744..86154  
misc_feature      /note="assembly_name:Contig41  
                  clone_end:T7  
                  vector_side:left"  
                  .86255..186176  
misc_feature      /note="assembly_name:Contig42"  
                  .37022 c 37474 g 54612 t 1505 others  
  
BASE COUNT       55563 n 37022 c 37474 g 54612 t 1505 others  
ORIGIN  
Query Match      90.0%; Score 18; DB 42; Length 186176;  
Best Local Similarity 100.0%; Pred. No. 20;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0:  
  
QY               1 atcagaagacnqactca 18  
                |||||  
Db 50029 ATCAGAGACGACTCA 50046  
  
RESULT 13  
LOCUS            AC005040     189949 bp      DNA          PRI           21-DEC-1999  
DEFINITION       Homo sapiens BAC clone RP11-519H15 from 2, complete sequence.  
ACCESSION        AC005040  
VERSION          AC005040.2 GI:4508119  
KEYWORDS         HTG.  
SOURCE           human.  
ORGANISM         Homo sap:ens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
TITLE            1 (bases 1 to 189949)  
AUTHORS          Sulston,T.E. and Waterston,R.  
JOURNAL           Toward a complete human genome sequence  
REFERENCE         Genome Res. 8 (11), 1097-1108 (1998)  
MEDLINE          99063792.  
REFERENCES        2 (bases 1 to 189949)  
AUTHORS          Madsen,C , Bauer,C. and Eldred,J.  
TITLE            The sequence of Homo sapiens BAC clone RP11-519H15  
JOURNAL           Unpublished  
AUTHORS          3 (bases 1 to 189949)  
TITLE            Waterston,R.H.  
AUTHORS          Direct Submission  
JOURNAL           Submitted (12-JUN-1998) Genome Sequencing Center, Washington  
REFERENCE         University School of Medicine, 4444 Forest Park Parkway, St. Louis,  
                  MO 63108, USA  
                  4 (bases 1 to 189949)  
AUTHORS          Waterston,R.H.  
TITLE            Direct Submission  
JOURNAL           Submitted (24-MAR-1999) Genome Sequencing Center, Washington  
REFERENCE         University School of Medicine, 4444 Forest Park Parkway, St. Louis,  
                  MO 63108, USA  
                  5 (bases 1 to 189949)  
REFERENCE
```

AUTHORS	Waterson, R.
TITLE	Direct Submission
JOURNAL	Submitted (22-OCT-1999) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
REFERENCE	6 (bases 1 to 189949)
AUTHORS	Waterson, R.
TITLE	Direct Submission
JOURNAL	Submitted (21-DEC-1999) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA

Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: <http://genome.wustl.edu/gsc>
Contact: saplens@wustl.wustl.edu
----- Summary Statistics -----
Center project name: H_NH0519H15

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality > 30): an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION: Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION: The RPc1-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Moon, P.Y., Zhao, B., Frengen, E., Tateo, M., Catanesi, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. *Genomics* 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute (<http://bacpac.med.buffalo.edu>)

VECTOR: pBACe3.6

NEIGHBORING SEQUENCE INFORMATION:
Actual start of this clone is at base position 1 of RP11-519H15;
Actual end is at base position 189949 of RP11-519H15.

The C at base position 22196 of RP11-519H15 is could possibly be a T.

The area from 183933 to 184208 in the BAC RP11-519H15 is covered by a PCR product from clone DNA.

FEATURES	Location/Qualifiers
source	1. .189949

```
repeat_region 1763. .2754 /rpt_family="MERL_type"
repeat_region 2755. 2837 /rpt_family="MTR"
misc_feature 4021. 4411 /note="match to EST AI239736 (NID:g3835133) qh43dl1.x1"
repeat_region 4559. 4625 /rpt_family="L2"
repeat_region 6439. 7759 /rpt_family="MER2_type"
repeat_region 8148. 8168 /rpt_family="(TAA)n"
repeat_region 8176. 8352 /rpt_family="Alu"
repeat_region 9587. 9893 /rpt_family="L2"
repeat_region 10018. 10157 /rpt_family="L2"
repeat_region 10716. 11030 /rpt_family="Alu"
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repeat_region 12029. 12087 /rpt_family="AT_rich"
repeat_region 12105. 12280 /rpt_family="L1"
repeat_region 13614. 13739 /rpt_family="MER2_type"
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repeat_region 15214. 15307 /rpt_family="AT_rich"
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repeat_region 15678. 15704 /rpt_family="AT_rich"
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repeat_region 16530. 16834 /rpt_family="Alu"
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repeat_region 24161. 24183 /rpt_family="Alu"
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repeat_region 24388. 24668 /rpt_family="Alu"
repeat_region 24689. 24791 /rpt_family="MTR"
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Best Local Similarity 100.0%; Pred. No. 20;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 atcagaagacagactca 18
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Db 30037 ATCAGAAGACAGACTCA 30020

RESULT 14
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LOCUS AR062114 Sequence 1 from patent US 5843678.
DEFINITION AR062114
ACCESSION AR062114
VERSION AR062114.1 GI:5989805
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 52)
AUTHORS Boyle,W.J.
TITLE Osteoprotegerin binding proteins
JOURNAL Patent: US 5843678-A 1 01-DEC-1998;
FEATURES Location/Qualifiers
source 1..52
BASE COUNT 13 a 15 c 8 g 16 t
ORIGIN

Query Match 87.0%; Score 17.4; DB 5; Length 52;
Best Local Similarity 94.7%; Pred. No. 37;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 tcagaagacagactcact 20
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Db 30 TCTGAAGACAGACTCCTACT 48

RESULT 15
HSJ744124 120515 bp DNA PRI 18-FEB-2000
LOCUS HSJ744124 Human DNA sequence from clone RP4-744124 on chromosome 6p12.1-21.2
DEFINITION Contains a novel gene (KIAA0646 (new zinc finger protein)), part of
a novel gene (similar to a novel human gene mapping to chromosome
22q13.3 similar to yeast ORF YOR070C, putative GTPase Activator),
ESTs, STSS, GSSs and a CpG Island, complete sequence.
ACCESSION AL096712
VERSION AL096712.20 GI:6425593

KEYWORDS HNG: Cpg Island; GTPase; KIAA0646; zinc finger.
SOURCE human
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS 1 (bases 1 to 120515)
TITLE Direct Submission
JOURNAL Tracey,A.
COMMENT Submitted (18-FEB-2000) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA. UK. E-mail enquiries: humqueye@sanger.ac.uk
requests: clonequest@sanger.ac.uk
On Nov 15, 1999 this sequence version replaced gi:6273550.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence has been finished according to sequence map criteria
as follows. An attempt is made to resolve all sequencing problems,
such as compressions and repeats, but not necessarily within known
annotated human repeat sequence elements (e.g. Alu). Where the
sequence is ambiguous, there is an annotation using the 'unsure'
feature key.
The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
Em., EMBL; Sw., SWISSPROT; Tr., TREMBL; Wp., WORMPEP; Information
on the WORMPEP database can be found at
http://www.sanger.ac.uk/Projects/C.elegans/wormpep RP4-744124 is
from the library RPCI-4 constructed at the Roswell Park Cancer
Institute by the group of Pieter de Jong. For further details see
http://bacpac.med.buffalo.edu/
VECTOR: pCYPAC2
This sequence is the entire insert of clone RP4-744124. This
sequence was generated from part of bacterial clone contigs of
human chromosome 6, constructed by the Sanger Centre Chromosome 6
Mapping Group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chr6.

FEATURES
source Location/Qualifiers
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/clone_lib="RPCI-4"
/map="p12.1-21.2"
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complement(519..890)
/note="match: GSS: Em:A0066699"
529..890
/note="match: GSS: Em:B41075"
complement(593..890)
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600..890
/note="match: GSS: Em:A0109548"
613..890
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4483..4874
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4965..5268
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5972..6247
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/codon_start=1
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Query Match 87.0% Score 17.4; DB 91; Length 120515;
Best Local Similarity 94.7% Pred. No. 44;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
DB 26200 ATCAGAGACAGCCTCAG 26218
OY 1 atcagaagacgactcac 19
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Search completed: November 1, 2000, 14:52:50
Job time: 16059 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: November 1, 2000, 14:55:35 ; Search time 141.28 Seconds
(without alignments)
793.247 Million cell updates/sec

Title: US-09-202-455-19

Perfect score: 741
Sequence: 1 ggcagatgacccatag.....aagtcgagatagattga 741

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Checked: 262060 seqs, 75620727 residues

Total number of hits satisfying chosen parameters: 524120

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- 1: Issued_Patents.NA.*
- 2: /cgn2_6/ptodata/1/ina/5A.COMB.seq.*
- 3: /cgn2_6/ptodata/1/ina/5B.COMB.seq.*
- 4: /cgn2_6/ptodata/1/ina/5C.COMB.seq.*
- 5: /cgn2_6/ptodata/1/ina/5D.COMB.seq.*
- 6: /cgn2_6/ptodata/1/ina/PCRN.COMB.seq.*
- 7: /cgn2_6/ptodata/1/ina/Backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	741	100.0	954	US-08-996-139-12	Sequence 12, Appl
2	522.2	70.5	1630	US-08-996-139-10	Sequence 10, Appl
3	520.6	70.3	2295	US-08-842-842-6	Sequence 6, Appl
4	69.4	9.4	1042	US-08-584-031-2	Sequence 2, Appl
5	69.4	9.4	1042	US-08-780-496-2	Sequence 2, Appl
6	69.4	9.4	1521	US-08-670-354-3	Sequence 3, Appl
7	69.4	9.4	1521	PCT-US96-10895-3	Sequence 3, Appl
8	69.4	9.4	1751	US-08-670-354-1	Sequence 1, Appl
9	69.4	9.4	1751	PCT-US96-10895-1	Sequence 1, Appl
10	57.6	7.8	1366	US-08-670-354-5	Sequence 5, Appl
11	57.6	7.8	1366	PCT-US96-10895-5	Sequence 5, Appl
12	37.4	5.0	390	US-08-584-031-3	Sequence 3, Appl
13	37.4	5.0	390	US-08-780-496-3	Sequence 3, Appl
14	37.4	5.0	7218	US-08-232-463-14	Sequence 14, Appl
15	35.6	4.8	59	US-08-842-842-5	Sequence 5, Appl
16	32.4	4.4	3095	5231168-1	Patent No. 5231168
17	32.4	4.4	2152	US-08-338-543-1	Sequence 1, Appl
18	30.6	4.1	3126	US-08-929-329-2	Sequence 2, Appl
19	30.6	4.1	3139	US-07-894-212A-1	Sequence 1, Appl
20	30.2	4.1	8387	US-08-532-814-1	Sequence 1, Appl
21	30.2	4.1	43795	US-08-742-185-101	Sequence 101, Appl
22	29.8	4.0	1440	US-08-836-022A-10	Sequence 10, Appl
23	29.8	4.0	1440	US-08-743-637B-174	Sequence 174, Appl
24	29.8	4.0	1440	US-08-526-840B-174	Sequence 174, Appl
25	29.2	3.9	3732	US-09-212-971-7	Sequence 7, Appl
26	29.2	3.9	591	US-08-788-954-1	Sequence 1, Appl

27	29	3.9	1374	1	US-08-093-372-3	Sequence 3, Appl
28	28.8	3.9	279	1	US-08-186-222-3	Sequence 3, Appl
29	28.8	3.9	1282	1	US-08-361-920-22	Sequence 22, Appl
30	28.8	3.9	1282	1	US-08-479-939-22	Sequence 22, Appl
31	28.8	3.9	1282	2	US-08-483-432-22	Sequence 22, Appl
32	28.8	3.9	1519	1	US-08-090-523-9	Sequence 9, Appl
33	28.8	3.9	1519	1	US-08-398-627-9	Sequence 9, Appl
34	28.8	3.9	1519	1	US-08-406-858-9	Sequence 9, Appl
35	28.8	3.9	1519	6	PCT-US91-04036-9	Sequence 9, Appl
36	28.8	3.9	1519	6	PCT-US94-05275-9	Sequence 9, Appl
37	28.8	3.9	1823	1	US-08-145-995A-1	Sequence 1, Appl
38	28.8	3.9	1823	2	US-08-451-747-1	Sequence 1, Appl
39	28.8	3.9	2730	2	US-08-339-129-1	Sequence 1, Appl
40	28.6	3.9	2417	1	US-08-011-398B-1	Sequence 1, Appl
41	28.6	3.9	2417	2	US-08-464-051-1	Sequence 1, Appl
42	28.6	3.9	2417	2	US-08-464-051-1	Sequence 1, Appl
43	28.6	3.9	2417	5	US-08-554-385-2	Sequence 2, Appl
44	28.6	3.9	9890	1	US-08-232-463-18	Sequence 18, Appl
45	28.4	3.8	52	3	US-08-842-842-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-08-996-139-12
; Sequence 12, Application US/08996139
; Patent No. 6017729
GENERAL INFORMATION:
APPLICANT: Anderson, Dirk M.
APPLICANT: Galibert, Laurent
APPLICANT: Maraskovsky, Eugene
TITLE OF INVENTION: Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation, Law Department
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/996,139
FILING DATE: 22 DECEMBER 1997
CLASSIFICATION:
APPLICATION DATA:
APPLICATION NUMBER: USSN 60/064,671
FILING DATE: 14 OCTOBER 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOC# NUMBER: 2851-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 954 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA

HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
LIBRARY:
CLONE: huRANKL (full length)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..951
US-08-996-139-12

Query Match 100.0%; Score 741; DB 5; Length 954;
Best Local Similarity 100.0%; Pred. No. 8e-233;
Matches 741; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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61 agactccatgaaatgcaatcttcaagacacactctggagagatcaataata 120
DB 274 AGACTCCAGAAATGCAATTTTCAAGACACACTCTGAGAGTCAAGATCAAAATTA 333
QY 121 ataccgtatcgttagaggaattaaacaggccttcaagagctgtgcaaaagaa 180
DB 334 ATACCTGATTCATGTAAGGAATTAACAGGCTTTCAAGAGACTGCAAAAGAAATTA 393
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DB 394 CAACATATGTTGATGATCAGACACATCAGAGCAAGAGAAAGCATGATGATGATG 453
QY 241 ttatgtctggcaagagagagagcttgagctcagcctttgtctatctcacta 300
DB 454 TTAGATCTGCGCAAGAGGAGCAAGCTTGAAGCTTGGCTTGTCTATCTCACTAATTA 513
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QY 361 ggttgagcagaatctcacaatgactttagcaatgaaataatagtttaacag 420
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QY 481 gctacagatctctcaactaagtgtgtaagcactcaaaacagacatcaaa 540
DB 694 GCTACAGATATCTTCAACTAATGATGATGATGATGATGATGATGATGATGATG 753
QY 541 tctcaccctgaatgaagaagagacacacagatattgttcagggaattctga 600
DB 754 TCTCATACCTGATGAAAGAGAGAACACCAAGTATGATGATGATGATGATGATG 813
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DB 814 TTTTATTCATTAACCTTGTGATTTTAAAGTTAGGCTTGGAGAGAAATCAACATC 873
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QY 721 aaagtgcagatatagatga 741
DB 934 AAAGTTCAGATATGATGATGA 954

RESULT 2
US-08-996-139-10
Sequence 10, Application US/08996139

Patent No. 6017729
GENERAL INFORMATION:
APPLICANT: Anderson, Dirk M.
APPLICANT: Galibert, Laurent
APPLICANT: Maraskovsky, Eugene
TITLE OF INVENTION: Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation, Law Department
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/996,139
FILING DATE: 22 DECEMBER 1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 60/064,671
FILING DATE: 14 OCTOBER 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2851-A
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SRO ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 1630 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Mus musculus
IMMEDIATE SOURCE:
LIBRARY:
CLONE: RANKL
FEATURE:
NAME/KEY: CDS
LOCATION: 3..884
US-08-996-139-10

Query Match 70.5%; Score 522.2; DB 5; Length 1630;
Best Local Similarity 82.6%; Pred. No. 3.9e-161;
Matches 612; Conservative 0; Mismatches 123; Indels 6; Gaps 1;

QY 1 ggcagatgagatcctaataatcagaagatgagcactcactgacttataagatttg 60
DB 153 GCGAGATGATCTCTAATAGAAATATCAGAAAGGACACACTGATTTATAGAAATTG 212
QY 61 agactccatgaaatgcaatcttcaagacacactctggagagatcaataata 120
DB 213 AGACTCCAGAAATGCAATTTTCAAGACACACTGATTTATAGAAATTG 266
QY 121 ataccgtatcgttagaggaattaaacaggccttcaagagctgtgcaaaagaa 180

Db 267 CTACCTGACTCCTGAGAGAGATGAACAAGCTTTCAAGGGGGCGGTGAGAGAAGACTG 326
QY 161 caacatcgttggatcacagacacatcagagagaagaagcgttggatggtcattg 240
Db 327 CAACACATGTTGGGGCCACAGCGCTTTCAGAGAGCTCCAGTATGATGAAAGGCTCATG 386
QY 241 tttagtctggcacaagaagagagagcttgaagctgagccttggccttcacatcattat 300
Db 387 TTGGATGTGGCCAGCAGAGCAAGCTTGAGGCCACATTTGACACCTCAACATCAAT 446
QY 301 ggcaccagacatcccatctggttcccaataaagtgatctgctctgtgacatgacg 360
Db 447 GGTGCGAGATGCCATCGGGGTCCCATAAAGTCACTCTCTCTGTGATCCACATGCA 506
QY 361 ggttggcgaagatctccaacatgactttagcaatggaataaataagtagtaacagat 420
Db 507 GCGTGGGCGCAAGATCTCTAAACATGACGTTAAAGCAAGGAACTAAAGGTTAAACAAAT 566
QY 421 ggcctttatctgtatgacaaatgttgcttgcacatcagaatcagaagaccta 480
Db 567 GCGTCTATTAACCTGTACGCCCAACATTTGCTTGCGCATCATGAACATCGGAAACGTA 626
QY 481 gctacagagatcctcaactaatgtgtacgtcactaaacacagacatcccaagt 540
Db 627 CCTACAGACTATCTTCAGCTGATGGTGTATGTCTTAAACAGCATCAAAATCCCAAT 686
QY 541 tctacaccctgatgaagaagagagacaaagtatttggcaggaatctgaatccat 600
Db 687 TCTCATTAACCTGATGAAGAGAGAGAGACAGAAACTGCTGGGCAATCTGAATTCAC 746
QY 601 tttattccataaagttgtgtgatttttaagttacggtctcggagaggaataacagcacc 660
Db 747 TTTTATTCATAAAGTTGGGGGATTTTCAAGCTCCGAGCTGGTGAATAAATTAACAT 806
QY 661 gaggtctcaaccctcctactgtgacgcgatacgaagatgacacatcattgggagcttt 720
Db 807 CAGGTGTCAACCTTCCCTGCTGTGATCCGATCAAGATGCCAGTACTTTGGGCTTTC 866
QY 721 aaagtcgagatagattga 741
Db 867 AAAGTCAAGACATAGACTGA 887

RESULT 3
US-08-842-842-6
; Sequence 6, Application US/08842842
; Patent No. 5843678
GENERAL INFORMATION:
APPLICANT: Boyle, William J.
TITLE OF INVENTION: OSTEOPROTEGERIN BINDING PROTEINS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
STREET: 1840 Dehavilland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91230-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/842.842
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-451
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 2295 base pairs

TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 158..1105
US-08-842-842-6

Query Match 70.3%; Score 520.6; DB 3; Length 2295;
Best Local Similarity 82.5%; Pred. No. 1.5e-160;
Matches 611; Conservative 0; Mismatches 124; Indels 6; Gaps 1.

QY 1 ggcgagatggatccttaataagatcagaagaatggcaactcactgattatgaatttg 60
Db 374 GCGAGATGGATCTTAAAGATATACAGAAACACACACTACTGCTTTATGAAATCCG 433
QY 61 agactccatgaataagcagattttcaagacacactctggagagatcaagatacaaat 120
Db 434 AGACTCCATGAATAAGCAGGTTTGAGAGACTGACTGTGAGAGTGAAGACAC-----A 487
QY 121 ataccgtatctatgtaggaatlaaacagccttcaagagcgtgtgcaaaaggaat 180
Db 488 CTACCTGACTCCTGAGAGAGATGAACAAGCTTTCAAGGGGGCCGTGAGAGAAGACTG 547
QY 181 caacatcgttggatcacagacacatcagagagaagaagcgttggatggtcattg 240
Db 548 CAACACATGTGGGGCCACAGCGCTTCTCAGAGACTCCAGTATGATGAAAGGCTCATG 607
QY 241 tttagtctggcacaagaagagagagcttgaagctcagccttggccttcacatcattat 300
Db 608 TTGGATGTGGCCAGCAGAGCAAGCTTGAGGCCACATTTGACACCTCAACATCAAT 667
QY 301 ggcaccagacatcccatctggttcccaataaagtgatctgctctgtgacatgacg 360
Db 668 GGTGCGAGATGCCATCGGGGTCCCATAAAGTCACTCTCTCTGTGATCCACATGCA 727
QY 361 ggttggcgaagatctccaacatgactttagcaatggaataaataagtagtaacagat 420
Db 728 GCGTGGGCGCAAGATCTCTAAACATGACGTTAAAGCAAGGAACTAAAGGTTAAACAAAT 787
QY 421 ggcctttatctgtatgacaaatgttgcttgcacatcagaatcagaagaccta 480
Db 788 GCGTCTATTAACCTGTACGCCCAACATTTGCTTGCGCATCATGAACATCGGAAACGTA 847
QY 481 gctacagagatcctcaactaatgtgtacgtcactaaacacagacatcccaagt 540
Db 848 CTTACAGACTATCTTCAGCTGATGGTGTATGTCTTAAACAGCATCAAAATCCCAAT 907
QY 541 tctacaccctgatgaagaagagagacaaagtatttggcaggaatctgaatccat 600
Db 908 TCTCATTAACCTGATGAAGAGAGAGAGACAGAAACTGCTGGGCAATCTGAATTCAC 967
QY 601 tttattccataaagttgtgtgatttttaagttacggtctcggagaggaataacagcacc 660
Db 968 TTTTATTCATAAAGTTGGGGGATTTTCAAGCTCCGAGCTGGTGAATAAATTAACAT 1027
QY 661 gaggtctcaaccctcctactgtgacgcgatacgaagatgacacatcattgggagcttt 720
Db 1028 CAGGTGTCAACCTTCCCTGCTGTGATCCGATCAAGATGCCAGTACTTTGGGCTTTC 1087
QY 721 aaagtcgagatagattga 741
Db 1088 AAAGTCAAGACATAGACTGA 1108

RESULT 4
US-08-584-031-2
; Sequence 2, Application US/08584031A
; Patent No. 6030945
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.

```

1  TITLE OF INVENTION: APO-2 LIGAND
2
3  FILE REFERENCE: 11669.22US03
4
5  CURRENT APPLICATION NUMBER: US/08/584,031A
6
7  CURRENT FILING DATE: 1996-01-09
8
9  NUMBER OF SEQ. ID NOS: 17
10
11  SOFTWARE: Patentin Ver. 2.0
12
13  SEQ. ID NO. 2
14
15  LENGTH: 1042
16
17  TYPE: DNA
18
19  ORGANISM: Homo sapiens
20
21  IS-06-364-031-2

```

Query Match	9.4%	Score	69.4	DB	5	Length	1042
Best Local Similarity	51.9%	Pred	No.3.8e-13				
Matches	182	Conservative	0	Mismatches	166	Indels	3
						Gaps	1

[illegible]

RESULT 5
US-08-780-496-2
Sequence 2, Application US/08780496
Patent No. 6046048
GENERAL INFORMATION:
APPLICANT: Avi Ashkenazi, Anan Chuncharapai, Kyung Jin Kim
TITLE OF INVENTION: Apo-2 Ligand
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/780,496
FILING DATE: 08-Jan-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Maerschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P0978P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5416
TELEFAX: 415/952-9881

```

; TELE# 910/371-7168
; INFORMATION FOR SEQ ID: 2
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1042 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
;
US-08-780-496-2

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Query Match	9.4%	Score 69.4;	DB 5;	length 1042;
Best Local Similarity	51.9%	Pred. No. 3.8e-13;		
Matches 102;	Conservative	0;	Mismatches 166;	Indels 3; Gaps 1;

QY	378	caacatgacatttgcgaatggaaaacacatcaattgtaacacagatgtgcttatcccgta	433
Db	585	CAACTTGGACCTTGAGGAATGGTGAACGTGTCATCCATGAAAAAGGTTTACTACATCTA	644
QY	438	tgcacacatttgccttgcacatcatgaaacttcagagagactagctacagaatctctca	497
Db	645	TTCCCAAAACATACCTTTTCATTTCAGGAGGAATATAAGA--AAACCAAAAGACGAA	701
QY	498	actaatggtgtaacgtcgaataaacacagcatcaaaatcccaagttctcataccctgatgaa	557
Db	702	ACAAATGGTCCAAATATATTTCAAAATACACAAGTTATTCGACCCCTTATTTGTGATGAA	761
QY	558	aggaggaagcncacaaatatttggtcaaggaatcttcgaatccattttatccataaacgt	617
Db	762	AAgTCTCTGAATATAGTTTGTGTCTAAAGAATGACGAATATGAGACTTATTCACATCTATCA	821
QY	618	tggatgatttttaagttacgctcgtgagaggaataatcagcatcagtcaggltctccacccctc	677
Db	822	AGGGGGAAATATTGAGCTTAAAGAAAATGACAGAAATTTTGTCTCTGAACAAATGAGCA	881
QY	678	cttaactgatccgagtcacgagtcagataactttggggcctttaaattg	728
Db	882	CTTGATTAAGACATGGACATGAAGCCAGTTTTCGTGGGGCCCTTTTAAATGG	932

RESULT 6
: US-08-670-354-3
: Sequence 3, Application US/08670354
: Patent No. 5763223
: GENERAL INFORMATION:
: APPLICANT: Steven R. Wiley and
: APPLICANT: Raymond G. Goodwin.
: TITLE OF INVENTION: Cytokine That Induces Apoptosis
: NUMBER OF SEQUENCES: 9
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
: STREET: 51 University Street
: CITY: Seattle
: STATE: WA
: COUNTRY: USA
: ZIP: 98101
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: Apple Macintosh
: OPERATING SYSTEM: Apple 7.5.2
: SOFTWARE: Microsoft Word, Version 6.0.1
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/570.354
: FILING DATE: 25-JUN-1996
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/496,632
: FILING DATE: 29-JUN-1995
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/548,368
: FILING DATE: 01-NOV-1995
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:

```

NAME: Anderson, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2835-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1521 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: HuAIC-dv
FEATURE:
NAME/KEY: CDS
LOCATION: 78..383
US-08-670-354-3

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Query Match          9.4%; Score 69.4; DB 2; Length 1521;
Best Local Similarity 51.9%; Pred. No. 4.6e-13;
Matches 182; Conservative 0; Mismatches 166; Indels 3; Gaps 1;

```

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QY 378 caccatgaactttaagcaagaaactaagtaacaggaagctttactactga 437
DB 424 CAACCTTGCACTTGAGGAAGGTCGACTGTCATCCATGAAAAAGGTTTACTACATCA 483
QY 438 tgcacacatttccttcgcacatcatgaactcagagacctaagctacagagatctca 497
DB 484 TTCCCAACATCTTTCGATTTCAGAGAGAAATATAAGA---AAACACAAGAACACACA 540
QY 498 actaatggtgtaacgtactcaaaacagcatcaaatcccaagttcctcaacctgatga 557
DB 541 ACAAAAGGTCACATATATTACAAATACACAAGTTATCCTGACCCTATATTGTTGATGAA 600
QY 558 agagagaagcaccagaatattgtgcaggaattctgaattccattttatccataaagt 617
DB 601 AAGTGCTAAGAAATAGTTGTTGGTCTTAAGATGCAAGATATGCACTATATTCATCTATCA 660
QY 618 tggtagatttttaagttacgctcgtgagagaaatcagacatcagagctcacaacctc 677
DB 661 AAGGGGAATATTGAGCTTAAGGAATAATGACAGAAATTTTGTTCGTAAACAATAGACA 720
QY 678 cttaactgataccgatacagatgacacatactttgggcttttaagttcg 728
DB 721 CTGTATAGACATGACCATGAAACCGAGTTTTCGGGGCCTTTTATGTTGG 771

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```

RESULT 7
PCT-US96-10895-3
Sequence 3, Application PC/TUS9610895
GENERAL INFORMATION:
APPLICANT: Immunex Corporation.
TITLE OF INVENTION: Cytokine That Induces Apoptosis
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.5.2
SOFTWARE: Microsoft Word, Version 6.0.1
CURRENT APPLICATION DATA:

```

```

APPLICATION NUMBER: PCT/US96/10895
FILING DATE: 25-JUN-1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/496,632
FILING DATE: 29-JUN-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/548,368
FILING DATE: 01-NOV-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Anderson, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2835-WO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1521 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: HuAIC-dv
FEATURE:
NAME/KEY: CDS
LOCATION: 78..383
PCT-US96-10895-3

```

```

Query Match          9.4%; Score 69.4; DB 6; Length 1521;
Best Local Similarity 51.9%; Pred. No. 4.6e-13;
Matches 182; Conservative 0; Mismatches 166; Indels 3; Gaps 1;

```

```

QY 378 caccatgaactttaagcaagaaactaagtaacaggaagctttactactga 437
DB 424 CAACCTTGCACTTGAGGAAGGTCGACTGTCATCCATGAAAAAGGTTTACTACATCA 483
QY 438 tgcacacatttccttcgcacatcatgaactcagagacctaagctacagagatctca 497
DB 484 TTCCCAACATCTTTCGATTTCAGAGAGAAATATAAGA---AAACACAAGAACACACA 540
QY 498 actaatggtgtaacgtactcaaaacagcatcaaatcccaagttcctcaacctgatga 557
DB 541 ACAAAAGGTCACATATATTACAAATACACAAGTTATCCTGACCCTATATTGTTGATGAA 600
QY 558 agagagaagcaccagaatattgtgcaggaattctgaattccattttatccataaagt 617
DB 601 AAGTGCTAAGAAATAGTTGTTGGTCTTAAGATGCAAGATATGCACTATATTCATCTATCA 660
QY 618 tggtagatttttaagttacgctcgtgagagaaatcagacatcagagctcacaacctc 677
DB 661 AAGGGGAATATTGAGCTTAAGGAATAATGACAGAAATTTTGTTCGTAAACAATAGACA 720
QY 678 cttaactgataccgatacagatgacacatactttgggcttttaagttcg 728
DB 721 CTGTATAGACATGACCATGAAACCGAGTTTTCGGGGCCTTTTATGTTGG 771

```

```

RESULT 8
US-08-670-354-1
Sequence 1, Application US/08670354
Patent No. 5763223
GENERAL INFORMATION:
APPLICANT: Steven R. Wiley and
Raymond G. Goodwin.
TITLE OF INVENTION: Cytokine That Induces Apoptosis

```



```

OY 498 actaatggtgacgtcactaaacaaacagcatcaaaatcccaagttctcataccctgaagaa 557
Db 699 ACAATGTCCTCAATATATTTCACAAATACACAAAGTTATCTCGACCCTATATTGTTGAAGAA 758
OY 558 agaggaagacccaagatattggtcagggaattctgaattccattttattccataaacgt 617
Db 759 AAGTCCTGGAATAGTTGTTGGTCTTAAAGATGCAGAAATATGAGACTATTCATTCATCTATCA 818
OY 618 tggaggatttttaagttaacggtctgtaaggaagaatacgaatcgaggtctccaaacctc 677
Db 819 AGGGGGAATATTTCAGCTTAAGAAAAATGACAGAAATTTGTTCTCTTAACAATGAGCA 878
Db 879 CTGATATACATGACATGACATGAGCAGCATTTTTCGGGGCCTTTTAAGTTGG 929

LT 10
8-670-354-5
: Sequence 5, Application US/08670354
: Patent No. 5763223
:
: GENERAL INFORMATION:
: APPLICANT: Steven R. Wiley and
: APPLICANT: Raymond G. Goodwin.
: TITLE OF INVENTION: Cytokine That Induces Apoptosis
: NUMBER OF SEQUENCES: 9
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
: STREET: 51 University Street
: CITY: Seattle
: STATE: WA
: COUNTRY: USA
: ZIP: 98101
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: Apple Macintosh
: OPERATING SYSTEM: Apple 7.5.2
: SOFTWARE: Microsoft word, Version 6.0.1
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/670,354
: FILING DATE: 25-JUN-1996
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/496,632
: FILING DATE: 29-JUN-1995
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/548,368
: FILING DATE: 01-NOV-1995
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Anderson, Kathryn A.
: REGISTRATION NUMBER: 32,172
: REFERENCE/DOCKET NUMBER: 2835-B
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (206) 587-0430
: TELEFAX: (206) 233-0644
: TELEX: 756822
:
: INFORMATION FOR SEQ ID NO: 5:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1366 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA to mRNA
: HYPOTHEICAL: NO
: ANTI-SENSE: NO
: IMMEDIATE SOURCE:
: CLONE: MuAIC
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 47..919

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```

US-08-670-354-5
Query_Match 7.8%; Score 57.6; DB 2; Length 1366;
Best Local Similarity 49.7%; Pred. No. 3.1e-09;
Matches 187; Conservative 0; Mismatches 174; Indels 15; Gaps 1.

Qy 374 tttccaacatgcttttggcaatggaataactaatatgatatcagatgcttttattacc 433
Db 549 tcaaccagatgctcttttgggaatggaagacctgtcatcgagagggcctgtattaca 608
Qy 434 tgtatgcacaacttggcttgcacatcgaacttcaggagacctca----- 480
Db 609 tctatttcccaacatcatttccgattttcaggaagcttgaagaccttccaagatgcttca 668
Qy 481 --gtcacagagatcttcaactaatgylgtacgtcactaaacccagcatcaaatccca 538
Db 669 aggacaagatgagAACCAACAGCTGTCATACATCTCAAGTACACAGCAGTATCCGG 728
Qy 539 gtctcacaacctgttgaaggaggaagcacaagaatgtgtcagggaattctgaattcc 598
Db 729 atcccatagtgctcatgaaagaccgccagaaacagctgttgcacagatgccagatagc 788
Qy 599 atttattcccaaacgctgtgtgatttttaagtttagcgtcagaggaatacaga 658
Db 788 gactgtactccatctatcagggagatttctgagcttaaaaaaaaaaaTGACAGATTTTG 848
Qy 659 tcgaaggtcccaacccctcctacttgatcggatcggatcagatgcaacatacttgggctt 718
Db 849 tttctgtgacaaatgaacatttgatgagacctgcatcaaaagccagctctttggagcct 908
Qy 719 ttaagtcgagatat 734
Db 909 ttttaattactaaat 924

RESULT 11
PCT-US96-10895-5
; Sequence 5, Application PC/TUS9610895
; GENERAL INFORMATION:
; APPLICANT: Immunex Corporation.
; TITLE OF INVENTION: Cytokine That Induces Apoptosis
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: Apple Macintosh
; SOFTWARE: Microsoft Word, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/10895
; FILING DATE: 25-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/496,632
; FILING DATE: 29-JUN-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/548,368
; FILING DATE: 01-NOV-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Anderson, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2835-WO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0450

```

TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1366 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: MUAIC
FEATURE:
NAME/KEY: CDS
LOCATION: 47...919
PCT-US96-10895-5

Query Match 7.8%; Score 57.6; DB 6; Length 1366;
Best Local Similarity 49.7%; Pred. No. 3.1e-09;
Matches 187; Conservative 0; Mismatches 174; Indels 15; Gaps 1;

QY 374 tctccacatgacttttagcaatggaaaactaatagtaatcaggatgctttattacc 433
DB 549 TCAACCAAGTGTCTTTAGAAATGAGAGCTGTGTCATGAGCAGGAGGCGCTGATTTACA 608
QY 434 tctatgcaaacatttgcttcgacatcatgaaacttcaggagacct----- 480
DB 609 TCTATCCCAACATATCTCCATTTTCAGGAGCTGAGAGCCGCTCCAGATGCTCTCAA 668
QY 481 --gtacagagatcttcacactatggtgtacgtcactaaacacagcatcaaatcccaa 538
DB 669 AGGACAAAGTGAACCAACAGCTGCTGTCATACATCTACAGATACACACTATCCGG 728
QY 539 gtctcataccctgtaagaggagagacacaaagtattgtcagggaattctgaattcc 598
DB 729 ATCCCATGATGCTCATGAAAGAGCGCCAGAAACAGCTGTGTGCCAGATGCCAGATAG 788
QY 599 attttatccataaagcttgatatttttaagttacggtcctgagggagaaatcagca 658
DB 789 GACTTACTCTCATCTATCAGGAGGATTTGTTGACCTAATAAAAAATGACAGATTTTTG 848
QY 659 tcgaagcttccaacccctctactactgagatcgatcagatcagacatacttgggctt 718
DB 849 TTTCTGTGACAAATGGAACATTGATGAGACTGATCAGAACAGCCAGCTTCTTGAGACT 908
QY 719 ttaagttcgagatat 734
DB 909 TTTTATTAATAATAAT 924

RESULT 12
US-08-584-031-3
Sequence 3, Application US/08584031A
Patent No. 6030945
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
TITLE OF INVENTION: APO-2 LIGAND
FILE REFERENCE: 11669.22US03
CURRENT APPLICATION NUMBER: US/08/584,031A
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO: 3
LENGTH: 390
TYPE: DNA
ORGANISM: Homo sapiens
US-08-584-031-3

Query Match 5.0%; Score 37.4; DB 5; Length 390;
Best Local Similarity 64.4%; Pred. No. 0.0066;

Matches 56; Conservative 0; Mismatches 31; Indels 0; Gaps 0;
QY 378 caacatgacttttagcaatggaaaactaatagtaatcaggatgctttattaccgta 437
DB 302 caacttgacattgaggaatggtgactggtcatcattgaaaagggttttactacatcta 361
QY 438 tgcacacattgcttcgacatcatga 464
DB 362 ttcccaaacatcttgcatttcagga 388

RESULT 13
US-08-780-496-3
Sequence 3, Application US/08780496
Patent No. 6046048
GENERAL INFORMATION:
APPLICANT: Avi Ashkenazi, Anan Chuntharapal, Kyung Jin Kim
TITLE OF INVENTION: APO-2 Ligand
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/780,496
FILING DATE: 08-Jan-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P0978P1
TELEPHONE: 415/225-5416
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 390 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
US-08-780-496-3

Query Match 5.0%; Score 37.4; DB 5; Length 390;
Best Local Similarity 64.4%; Pred. No. 0.0066;
Matches 56; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 378 caacatgacttttagcaatggaaaactaatagtaatcaggatgctttattaccgta 437
DB 302 CAACCTTGACACTTGAGGAATGTTGAACTGTCATCCATGAAAAAGGTTTACTACATCTA 361
QY 438 tgcacacattgcttcgacatcatga 464
DB 362 TTCCCAACATACTTTCGATTTCAGGA 388

RESULT 14
US-08-232-463-14/c
Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEFFELINGER, F.
APPLICANT: FALKNER, F. G.

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 1, 2000, 14:55:50 ; Search time 54.03 Seconds
(without alignments)
76.314 Million cell updates/sec

Title: US-09-202-455-17

Sequence: 1 AOMDPNRISDGTGHCYRIL.....LLDPDDATYFGAFKVRDID 246

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Total number of hits satisfying chosen parameters: 164575

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database:

- 1: Issued Patents.AA.*
- 2: /cgn2_6/ptodata/1/1aa/5A.COMB.pep.*
- 3: /cgn2_6/ptodata/1/1aa/5B.COMB.pep.*
- 4: /cgn2_6/ptodata/1/1aa/6.COMB.pep.*
- 5: /cgn2_6/ptodata/1/1aa/PCRTUS.COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the total being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1301	100.0	317	3	US-08-996-139-13
2	1116	85.8	294	3	US-08-996-139-11
3	1109	85.2	316	2	US-08-842-842-7
4	235.5	18.1	281	1	US-08-670-334-2
5	235.5	18.1	281	1	US-08-584-031-1
6	235.5	18.1	281	4	US-08-780-496-1
7	235.5	18.1	281	4	PCT-US96-10895-2
8	235	18.1	291	4	US-08-670-334-6
9	235	18.1	291	4	PCT-US96-10895-6
10	164.5	12.6	376	3	US-08-751-512-8
11	160	12.3	279	4	PCT-US95-00362-5
12	157	12.1	287	3	US-08-815-190A-16
13	150	11.5	261	1	US-07-940-605A-2
14	150	11.5	261	1	US-08-184-422-8
15	150	11.5	261	1	US-08-360-923A-2
16	150	11.5	261	1	US-08-446-922-4
17	150	11.5	261	1	US-08-431-055-4
18	150	11.5	261	2	US-08-690-096-2
19	150	11.5	261	2	US-08-249-189-12
20	150	11.5	261	2	US-08-484-624A-12
21	150	11.5	261	2	US-08-477-733B-12
22	150	11.5	261	3	US-08-763-995-2
23	150	11.5	261	3	US-09-088-913A-12
24	150	11.5	261	3	US-08-589-771B-8
25	150	11.5	261	4	PCT-US93-10034-4
26	150	11.5	273	1	US-08-446-922-11
27	150	11.5	273	2	US-08-249-189-21
28	150	11.5	273	2	US-08-484-624A-21

29	150	11.5	273	2	US-08-477-733B-21	Sequence 21, Appl
30	150	11.5	273	3	US-09-088-913A-21	Sequence 21, Appl
31	150	11.5	473	2	US-08-249-189-16	Sequence 16, Appl
32	150	11.5	473	2	US-08-484-624A-16	Sequence 16, Appl
33	150	11.5	473	2	US-08-477-733B-16	Sequence 16, Appl
34	150	11.5	473	3	US-09-088-913A-16	Sequence 16, Appl
35	149.5	11.5	281	3	US-08-649-100-9	Sequence 9, Appl
36	149.5	11.5	281	2	US-08-810-453-2	Sequence 2, Appl
37	149.5	11.5	281	3	US-08-815-190A-2	Sequence 2, Appl
38	149.5	11.5	281	4	PCT-US95-00362-2	Sequence 2, Appl
39	145.5	11.2	145	3	US-08-630-172-5	Sequence 5, Appl
40	145.5	11.2	378	3	US-08-630-172-21	Sequence 21, Appl
41	141.5	10.9	156	2	US-08-500-860A-36	Sequence 36, Appl
42	141	10.8	155	1	US-07-994-469A-94	Sequence 94, Appl
43	141	10.8	158	1	US-07-794-400-6	Sequence 6, Appl
44	141	10.8	158	1	US-07-994-469A-99	Sequence 99, Appl
45	141	10.8	158	1	US-08-397-470-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1
US-08-996-139-13
Sequence 13, Application US/08996139
Patent No. 6017729
GENERAL INFORMATION:
APPLICANT: Anderson, Dirk M.
APPLICANT: Galbert, Laurent
TITLE OF INVENTION: Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Immunex Corporation, Law Department
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: Apple Power Macintosh
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/996,139
FILING DATE: 22 DECEMBER 1997
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: USSN 60/064,671
FILING DATE: 14 OCTOBER 1997
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2851-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 317 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-996-139-13

102(e)
12-23-97

72-317
11

Query Match 100.0%; Score 1301; DB 3; Length 317;
Best Local Similarity 100.0%; Pred. No. 9.7e-139;
Matches 246; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AQMDPNRISEDTGTCIYRLRLHENAPODPTLESODTKLIPDSGRKQAFQGAQVOKEL 60
DB 72 AQMDPNRISEDTGTCIYRLRLHENAPODPTLESODTKLIPDSGRKQAFQGAQVOKEL 131
QY 61 OHIVSGHIRAKAWDGSMDLAKRSKLEAPFAHLITINATDIPSGSHKVSLSWYHDR 120
DB 132 OHIVSGHIRAKAWDGSMDLAKRSKLEAPFAHLITINATDIPSGSHKVSLSWYHDR 191
QY 121 GWAKISNMTFSGKLIYNODGFYLLYANICFRHHETSGDLATEYLQMLVYVTKTSIKIPS 180
DB 192 GWAKISNMTFSGKLIYNODGFYLLYANICFRHHETSGDLATEYLQMLVYVTKTSIKIPS 251
QY 181 SHTLKGGSTKYWGSNFEHFYSINVGFFKLRSGEISIEVSNPSLDDPDODATYFGAF 240
DB 252 SHTLKGGSTKYWGSNFEHFYSINVGFFKLRSGEISIEVSNPSLDDPDODATYFGAF 311
QY 241 KYRID 246
DB 312 KYRID 317

RESULT 2

US-08-996-139-11
Sequence 11, Application US/08996139
Patent No. 6017729

GENERAL INFORMATION:

APPLICANT: Anderson, Dirk M.
APPLICANT: Galibert, Laurent
APPLICANT: Maraskovsky, Eugene
TITLE OF INVENTION: Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation, Law Department
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA

ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/996,139
FILING DATE: 22 DECEMBER 1997

CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 60/064,671
FILING DATE: 14 OCTOBER 1997

PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997

PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996

ATTORNEY/AGENT INFORMATION:

NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2851-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:
LENGTH: 294 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-996-139-11

Query Match 85.8%; Score 1116; DB 3; Length 294;
Best Local Similarity 85.0%; Pred. No. 6.7e-118;
Matches 209; Conservative 14; Mismatches 21; Indels 2; Gaps 1;

QY 1 AQMDPNRISEDTGTCIYRLRLHENAPODPTLESODTKLIPDSGRKQAFQGAQVOKEL 60
DB 51 AQMDPNRISEDTGTCIYRLRLHENAPODPTLESODTKLIPDSGRKQAFQGAQVOKEL 108
QY 61 OHIVSGHIRAKAWDGSMDLAKRSKLEAPFAHLITINATDIPSGSHKVSLSWYHDR 120
DB 109 OHIVSGHIRAKAWDGSMDLAKRSKLEAPFAHLITINATDIPSGSHKVSLSWYHDR 168
QY 121 GWAKISNMTFSGKLIYNODGFYLLYANICFRHHETSGDLATEYLQMLVYVTKTSIKIPS 180
DB 169 GWAKISNMTFSGKLIYNODGFYLLYANICFRHHETSGDLATEYLQMLVYVTKTSIKIPS 228
QY 181 SHTLKGGSTKYWGSNFEHFYSINVGFFKLRSGEISIEVSNPSLDDPDODATYFGAF 240
DB 229 SHTLKGGSTKYWGSNFEHFYSINVGFFKLRSGEISIEVSNPSLDDPDODATYFGAF 288
QY 241 KYRID 246
DB 289 KYRID 294

RESULT 3

US-08-842-842-7
Sequence 7, Application US/08842842
Patent No. 5843678

GENERAL INFORMATION:

APPLICANT: Boye, William J.
APPLICANT: OSTEOPROTEGERIN BINDING PROTEINS
TITLE OF INVENTION: OSTEOPROTEGERIN BINDING PROTEINS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
STREET: 1840 Dehaven Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA

ZIP: 91320-1789

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/842,842
FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-451

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:
LENGTH: 316 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-842-842-7

Query Match 85.2%; Score 1109; DB 2; Length 316;
Best Local Similarity 84.6%; Pred. No. 4.7e-117;
Matches 208; Conservative 14; Mismatches 22; Indels 2; Gaps 1;

QY 1 AQMDPNRISEDTGTCIYRLRLHENAPODPTLESODTKLIPDSGRKQAFQGAQVOKEL 60
DB 73 AQMDPNRISEDTGTCIYRLRLHENAPODPTLESODTKLIPDSGRKQAFQGAQVOKEL 130
QY 61 OHIVSGHIRAKAWDGSMDLAKRSKLEAPFAHLITINATDIPSGSHKVSLSWYHDR 120

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Db 131 OHVGPORFSCAPAMMESWLDVAORGPKEQPRHHLTINASIPSGSHKATLSSWYDR 190
QY 121 GWAKISNMTFSGKLIYNODGFYLLANICFRHHETSGDLATEYLQMLVYVTKTSIKIPS 180
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 191 GWAKISNMTLSNGKLRVQDGFYLLANICFRHHETSGSVPTDYLQMLVYVTKTSIKIPS 250
QY 181 SHTLMKGGSTYWGSGNSEFHFYSINVGFFKLRSGEISIEVSNPSLDDPDATYFGAF 240
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 251 SHNLMKGGSTYWGSGNSEFHFYSINVGFFKLRSGEISIEVSNPSLDDPDATYFGAF 310
QY 241 KYRDID 246
    |||||
Db 311 KYRDID 316

```

RESULT 4

```

US-08-670-354-2
: Sequence 2, Application US/08670354
: Patent No. 5763223
: GENERAL INFORMATION:
: APPLICANT: Steven R. Wiley and
: APPLICANT: Raymond G. Goodwin.
: TITLE OF INVENTION: Cytokine That Induces Apoptosis
: NUMBER OF SEQUENCES: 9
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
: STREET: 51 University Street
: CITY: Seattle
: STATE: WA
: COUNTRY: USA
: ZIP: 98101
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: Apple Macintosh
: OPERATING SYSTEM: Apple 7.5.2
: SOFTWARE: Microsoft Word, Version 6.0.1
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/670.354
: FILING DATE: 25-JUN-1996
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/496,632
: FILING DATE: 29-JUN-1995
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/548,368
: FILING DATE: 01-NOV-1995
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Anderson, Kathryn A.
: REGISTRATION NUMBER: 32,172
: REFERENCE/DOCKET NUMBER: 2835-B
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (206) 587-0430
: TELEFAX: (206) 233-0644
: TELEX: 756822
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 281 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-670-354-2

```

```

Query Match 18.1%; Score 235.5; DB 1; Length 281;
Best Local Similarity 25.3%; Pred. No. 1.7e-18;
Matches 65; Conservative 51; Mismatches 98; Indels 43; Gaps 9;
QY 6 NRISDGTGHCIRILRLHENDADFDLTLESODTKLIPSCSRRIKQAFGAVGKELQHYG 65
    ::||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 47 DKYSKSGIACF-----LKEQ-----DSYWDPNDESMNSPCWQVW-----QLRQLYR 89

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QY 66 SQHRAEKAWYDGSWLDLAKRSKLEAQP-----AHLT-----INATDIPSGSHK 110
Db 90 KMLRTSEETI-----STVQEKQONISPLVREGRQRYAAHITGRGSRNTLSSPSNKE 144
    ::||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 111 VSL-----SSWYHDR-GWAKISNMTFSGKLIYNODGFYLLANICFRHHETSGDLATEYL 165
    ::||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 145 KALGRKINSWSSSGHSFSLNHLRNGELVYHEKGFYIYSQTYFRQDEIKENTKNDK 204
QY 166 QLMVYVTKTSIKIPSSHTLMKGGSTKYWGSGNSEFHFYSINVGFFKLRSGEISIEVSNP 225
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 205 QMVOYIYKYT--SYDPDILMMSARNSCKMADEYGLYSIYGGLFELKENDRIEVSVTNE 263
QY 226 SLDDPDATYFGAFKY 242
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 264 HLIDMDHEASFFGAFLV 280

```

RESULT 5

```

US-08-584-031-1
: Sequence 1, Application US/08584031A
: Patent No. 6030945
: GENERAL INFORMATION:
: APPLICANT: Ashkenazi, Avi J.
: TITLE OF INVENTION: APO-2 LIGAND
: FILE REFERENCE: 11669.22US03
: CURRENT APPLICATION NUMBER: US/08/584,031A
: CURRENT FILING DATE: 1996-01-09
: NUMBER OF SEQ ID NOS: 17
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 1
: LENGTH: 281
: TYPE: PRT
: ORGANISM: Homo sapiens
: US-08-584-031-1

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Query Match 18.1%; Score 235.5; DB 3; Length 281;
Best Local Similarity 25.3%; Pred. No. 1.7e-18;
Matches 65; Conservative 51; Mismatches 98; Indels 43; Gaps 9;
QY 6 NRISDGTGHCIRILRLHENDADFDLTLESODTKLIPSCSRRIKQAFGAVGKELQHYG 65
    ::||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 47 DKYSKSGIACF-----LKEQ-----DSYWDPNDESMNSPCWQVW-----QLRQLYR 89

```

```

QY 66 SQHRAEKAWYDGSWLDLAKRSKLEAQP-----AHLT-----INATDIPSGSHK 110
Db 90 KMLRTSEETI-----STVQEKQONISPLVREGRQRYAAHITGRGSRNTLSSPSNKE 144
    ::||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 111 VSL-----SSWYHDR-GWAKISNMTFSGKLIYNODGFYLLANICFRHHETSGDLATEYL 165
    ::||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 145 KALGRKINSWSSSGHSFSLNHLRNGELVYHEKGFYIYSQTYFRQDEIKENTKNDK 204
QY 166 QLMVYVTKTSIKIPSSHTLMKGGSTKYWGSGNSEFHFYSINVGFFKLRSGEISIEVSNP 225
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 205 QMVOYIYKYT--SYDPDILMMSARNSCKMADEYGLYSIYGGLFELKENDRIEVSVTNE 263
QY 226 SLDDPDATYFGAFKY 242
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 264 HLIDMDHEASFFGAFLV 280

```

```

RESULT 6
: US-08-780-496-1
: Sequence 1, Application US/08780496
: Patent No. 6046048
: GENERAL INFORMATION:
: APPLICANT: Avi Ashkenazi, Anan Chuntharapai, Kyung Jin Kim
: TITLE OF INVENTION: Apo-2 Ligand
: NUMBER OF SEQUENCES: 8
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Genentech, Inc.
: STREET: 460 Point San Bruno Blvd

```

CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/780.496
FILING DATE: 08-Jan-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Maichang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P0978P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5416
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 281 amino acids
TYPE: Amino acid
TOPOLOGY: Linear
US-08-780-496-1

Query Match 18.1%; Score 235.5; DB 3; Length 281;
Best Local Similarity 25.3%; Pred. No. 1,7e-18;
Matches 65; Conservative 51; Mismatches 98; Indels 43; Gaps 9;

QY 6 NRISDGHCHYRILRLHENAEDFDTLESODTKLIPDSRRIRKQAFQGAOKELQHYVG 65
DB 47 DKYSKSGIACF-----LKED-----DSYWDPNDESMNSPCQVW-----OLRQLVLR 89
QY 66 SQHIAEAMVDSWLDLAKRSKLEAOPF-----AHLT-----INATDIPSGSHK 110
DB 90 KMLITSEETI-----STVQEKQONISPLVREGRFORVAHAHITGRGNSNTLSSPSKNE 144
QY 111 VSL-----SSWYHDR-GWAKISNMTFSNGKLIYNODGFYLLYANICFRHHETSGDLATEYL 165
DB 145 KALGRKINSWESSRSGHSLNLHRLNGELVTHEKGFYIYSQTFPRQEELKENTKNDK 204
QY 166 QLMAYVTITSLIPSSHTLMKGGSTKRWGSEHFHYSINVGCFKRLSGEELISIEVSNP 225
DB 205 QMVOYIYKYT-SYDPPIILMKARSNCWCKDAEYGLYSIYOGIFELKENDRIEVSATNE 263
QY 226 SLDDPDODATYGAFAKV 242
DB 264 HLIDMDHEASFFGAPLV 280

RESULT 7
PCT-US96-10895-2
Sequence 2, Application PC/TUS9610895
GENERAL INFORMATION:
APPLICANT: Immunex Corporation.
TITLE OF INVENTION: Cyclokin That Induces Apoptosis
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.5.2
SOFTWARE: Microsoft Word, Version 6.0.1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10895
FILING DATE: 25-JUN-1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/496,632
FILING DATE: 29-JUN-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/548,368
FILING DATE: 01-NOV-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Anderson, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2835-WO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 281 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US96-10895-2

Query Match 18.1%; Score 235.5; DB 4; Length 281;
Best Local Similarity 25.3%; Pred. No. 1,7e-18;
Matches 65; Conservative 51; Mismatches 98; Indels 43; Gaps 9;

QY 6 NRISDGHCHYRILRLHENAEDFDTLESODTKLIPDSRRIRKQAFQGAOKELQHYVG 65
DB 47 DKYSKSGIACF-----LKED-----DSYWDPNDESMNSPCQVW-----OLRQLVLR 89
QY 66 SQHIAEAMVDSWLDLAKRSKLEAOPF-----AHLT-----INATDIPSGSHK 110
DB 90 KMLITSEETI-----STVQEKQONISPLVREGRFORVAHAHITGRGNSNTLSSPSKNE 144
QY 111 VSL-----SSWYHDR-GWAKISNMTFSNGKLIYNODGFYLLYANICFRHHETSGDLATEYL 165
DB 145 KALGRKINSWESSRSGHSLNLHRLNGELVTHEKGFYIYSQTFPRQEELKENTKNDK 204
QY 166 QLMAYVTITSLIPSSHTLMKGGSTKRWGSEHFHYSINVGCFKRLSGEELISIEVSNP 225
DB 205 QMVOYIYKYT-SYDPPIILMKARSNCWCKDAEYGLYSIYOGIFELKENDRIEVSATNE 263
QY 226 SLDDPDODATYGAFAKV 242
DB 264 HLIDMDHEASFFGAPLV 280

RESULT 8
US-08-670-354-6
Sequence 6, Application US/08670354
Patent No. 5763223
GENERAL INFORMATION:
APPLICANT: Steven R. Wiley and
APPLICANT: Raymond G. Goodwin.
TITLE OF INVENTION: Cyclokin That Induces Apoptosis
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh

```

OPERATING SYSTEM: Apple 7.5.2
SOFTWARE: Microsoft Word, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/670.354
FILING DATE: 25-JUN-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/496,632
FILING DATE: 29-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/548,368
FILING DATE: 01-NOV-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Anderson, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2835-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 291 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-670-354-6

```

```

Query Match 18.1%, Score 235, DB 1, Length 291;
Best Local Similarity 25.6%, Pred. No. 2.1e-18;
Matches 72; Conservative 47; Mismatches 84; Indels 78; Gaps 12;

```

```

QY 2 QMDPRISDEGHICIRILRLHENDFQDTLESQDTKLIPDSCKRIK----- 49
DB 48 QLDN-YKISGLACFSK-----TDEDFWST---DGETLNPPCLQVVRKQLYQLEEVTL 97
QY 50 QAFQ-----GAVQKELQHVSGHIRAEKAWDGSWLDLAKRSKLE 90
DB 98 RFFQOTISTVPEKQSTPLPRGGRPKYKAHITGTR-RKSNALI-----PISDKGTL 151
QY 91 AQFPAHLTINADIPSGSHKYSLSWYHDR-GWAKISNMTFSNGKLIVNODGFYLYANI 149
DB 152 GQ-----KIESWESSRKGHSLNHYLFNNGELVIEQEGLYIYSQT 192
QY 150 CRRHETSQDLATEYL-----QLMYVYVTKTSIKIPSSHTLMGSGTKYSGNSEFHF 201
DB 193 YRFQEAED--ASKWVSKDKVTKQLYQIYKYT-STDPPIYLMKSARNSCWSDAEYGL 249
QY 202 YSINVGFELKRSGEISIEVSNPILDPDODATYFGAFKV 242
DB 250 YSIYGGFLFELKKNDRIYVSTNEHLMDDQASFFGAFLI 290

```

```

RESULT 9
PCT-US96-10895-6
Sequence 6, Application PC/TUS9610895
GENERAL INFORMATION:
APPLICANT: Immunex Corporation.
TITLE OF INVENTION: Cytokine That Induces Apoptosis
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh

```

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OPERATING SYSTEM: Apple 7.5.2
SOFTWARE: Microsoft Word, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10895
FILING DATE: 25-JUN-1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/496,632
FILING DATE: 29-JUN-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/548,368
FILING DATE: 01-NOV-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Anderson, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2835-WO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 291 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US96-10895-6

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```

Query Match 18.1%, Score 235, DB 4, Length 291;
Best Local Similarity 25.6%, Pred. No. 2.1e-18;
Matches 72; Conservative 47; Mismatches 84; Indels 78; Gaps 12;

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```

QY 2 QMDPRISDEGHICIRILRLHENDFQDTLESQDTKLIPDSCKRIK----- 49
DB 48 QLDN-YKISGLACFSK-----TDEDFWST---DGETLNPPCLQVVRKQLYQLEEVTL 97
QY 50 QAFQ-----GAVQKELQHVSGHIRAEKAWDGSWLDLAKRSKLE 90
DB 98 RFFQOTISTVPEKQSTPLPRGGRPKYKAHITGTR-RKSNALI-----PISDKGTL 151
QY 91 AQFPAHLTINADIPSGSHKYSLSWYHDR-GWAKISNMTFSNGKLIVNODGFYLYANI 149
DB 152 GQ-----KIESWESSRKGHSLNHYLFNNGELVIEQEGLYIYSQT 192
QY 150 CRRHETSQDLATEYL-----QLMYVYVTKTSIKIPSSHTLMGSGTKYSGNSEFHF 201
DB 193 YRFQEAED--ASKWVSKDKVTKQLYQIYKYT-STDPPIYLMKSARNSCWSDAEYGL 249
QY 202 YSINVGFELKRSGEISIEVSNPILDPDODATYFGAFKV 242
DB 250 YSIYGGFLFELKKNDRIYVSTNEHLMDDQASFFGAFLI 290

```

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RESULT 10
US-08-751-512-8
Sequence 8, Application US/08751512
Patent No. 6001962
GENERAL INFORMATION:
APPLICANT: Ramer, J. Kevin
APPLICANT: Williams, Lewis T.
TITLE OF INVENTION: Modified FAS Ligands
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:

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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/751,512
FILING DATE: 15-NOV-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Murphy, Matthew B.
REGISTRATION NUMBER: 39,787
REFERENCE/DOCKET NUMBER: 02307K-071000S
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 376 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
8-751-512-8

Query Match 12.6%; Score 164.5; DB 3; Length 376;
Best Local Similarity 23.6%; Pred. No. 2.8e-10;
Matches 59; Conservative 39; Mismatches 89; Indels 63; Gaps 9;

QY 32 TLESODTKIPSCRIKAFQAGV-----QKELQIVSQ--HRAEKA 74
DB 151 TIASOPLSLRPACR--PAGGAVHTRGLDRLACLEHHHHHEFEFMPQDLHOKELA 207
QY 75 MYDGSMLDLAKRSKLEAQ-----PFAHLT--INATDIPSGSHKVSLSMYH 118
DB 208 ELRETSQMHNTASSLEKQGHPSPEPEKELKVAHLTKSNRSKP-----LEWED 259
QY 119 DRGMKISMNFTSNGELIYNODGFYLYANICFRHHTSGDLATEYLQMLVYTKISIKI 178
DB 260 TYGIVLSGVKKYKKGGLVNETGLFVYSKYVFRGQSCNN-----LPLSHKYVMNSKY 313
QY 179 PSSHTLMKGGSTKY-----WGSNFEHFYSINVGCFYLRGSELSIEVSNPSLDPQ 232
DB 314 PQDLVMECKMNSYCTGTGMWARRS-----YLGAVFMTSADHLVYVSELCLVNEBE 366
QY 233 DATYFAGKV 242
DB 367 SOTFFGLYKL 376

US95-00362-5
Sequence 5, Application PC/TUS9500362
GENERAL INFORMATION:
APPLICANT: IMMUNEX CORPORATION
TITLE OF INVENTION: Ligand That Binds Fas Antigen
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: US
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.1
SOFTWARE: Microsoft Word, Version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/00362
FILING DATE: 06-JAN-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/179,138
FILING DATE: 07-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/190,559
FILING DATE: 01-FEB-1994
ATTORNEY/AGENT INFORMATION:
NAME: Anderson, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2805-WO
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 279 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-00362-5

Query Match 12.3%; Score 160; DB 4; Length 279;
Best Local Similarity 25.9%; Pred. No. 5.7e-10;
Matches 50; Conservative 39; Mismatches 80; Indels 24; Gaps 8;

QY 56 VOKELQHT--VGSQHTRA---EKANVDSMLDLAKRSKLEQPFRAHLTINATDIPSGSHK 110
DB 105 LQKELAELEERTNOSLKYSSEKQIANPS---TPSEKKEPRSYAHLTGN-----PHS 153
QY 111 VSLT-SWYHDGMKISMNFTSNGELIYNODGFYLYANICFRHHTSGDLATEYLQMLV 169
DB 154 RSIPLMEDTYGTALISGVKKYKKGGLVNETGLFVYSKYVFRGQSCN---NOLNKKV 209
QY 170 YTKTSIKRIPSHHTLMKGGSTKYWSGNSEFHFYSINVGCFYLRGSELSIEVSNPSLDD 229
DB 210 YWRNS--KYPDVLVMECKRLNLYFR--TGQIWAHSSYLGAVFMTSADHLVYVSELCLV 266
QY 230 PQDLATYFAGKV 242
DB 267 FEESKTFGLYKL 279

RESULT 12
US-08-815-190A-16
Sequence 16, Application US/08815190A
Patent No. 6046310
GENERAL INFORMATION:
APPLICANT: Queen, Cary L.
APPLICANT: Schneider, William P.
APPLICANT: Vasquez, Maximiliano
TITLE OF INVENTION: Fas Ligand Fusion Proteins and Their
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/815,190A
FILING DATE: 11-MAR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/614,584
FILING DATE: 13-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 011823-0067100S

```

? TELECOMMUNICATIONS INFORMATION
? TELEPHONE: (415) 576-0200
? TELEFAX: (415) 576-0300
? INFORMATION FOR SEQ ID NO: 16:
? SEQUENCE CHARACTERISTICS:
?   LENGTH: 287 amino acids
?   TYPE: amino acid
?   TOPOLOGY: linear
?   MOLECULE TYPE: protein
?
US-08-815-190A-16

```

Query Match	12.1%	Score	157	DB 3:	Length	287;			
Best Local Similarity	23.0%	Pred. No.	1.3e-09;						
Matches	61;	Conservative	42;	Mismatches	104;	Indels	58;	Gaps	10

QY	5	PNRIBEDSTHIOIURLYRLNENAAEDPODTTLESQDTKLLIPRSCRRKJAFQOG-AVOK--ELQ	61
		54	PRMLDSDSFFLLYKSLIYDKSRMGOQGNF-----SCSVNHEMLNHNHYOKLSLS
QY	62	HIVSQ--HIRAKAMDGSWLDAKSKLEAO-----REAHLT--INATD	103
Db	104	PSKGOTFHLOKRELALEESTSQMNTASLEKQIGSPREKKELRYALITGKSNSRS	163
QY	104	IPSGSHKXLSLWSYHNRGMAKISMWTASNGKLIYNODGFYUYNIGOFNHNHSGDATE	163
Db	164	MP-----LEMEDTYGIVLLSGVTKKGGVILNETGLIFVUSKYVFRQOSCN-----	210
QY	164	YLQLMVYVTKTSIKIPSSHLLMKGSGTRY-----WSGNSBFHRYLSINVGFFFLRSGEE	217
Db	211	LPLSHKXUYNKMSKXPOQVLWMEKMKMSYCTGQMMARSS-----YLGAVFNLGADH	262
QY	218	ISIEVSNPSLDDPDODATYFCAFVY	242
Db	263	LYVNVSELSLVNFEESQTFEGLYVL	287

RESULT 13
 US-07-940-605A-2
 Sequence 2, Application US/079400605A
 Patent No. 5540926
 GENERAL INFORMATION:
 APPLICANT: ARUFFO, ALEJANDRO
 APPLICANT: HOLLENBAUGH, DIANE
 APPLICANT: LEDBETTER, JEFFREY A.
 TITLE OF INVENTION: SOLUBLE LIGANDS FOR CD40
 NUMBER OF SEQUENCES: 15
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Pennie & Edmonds
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10036-2711
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.255A
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/940,605A
 FILING DATE: 04-SEP-1992
 CLASSIFICATION: 530
 ATTORNEY/AGENT INFORMATION:
 NAME: Mistrock, S. Leslie
 REGISTRATION NUMBER: 16,872
 REFERENCE/DOCKET NUMBER: 562A-184
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212 790-9090
 TELEFAX: 212 869-8864/9741
 TELEX: 66141 PENNIE
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS: 2

```

; LENGTH: 261 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-07-940-605A-2

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Query Match	1.5%	Score 150;	DB 1;	Length 261;
Best Local Similarity	25.4%	Pred. No. 6.8e-09;		
Matches	58;	Conservative	43;	Mismatches 95;
			Indels	32;
			Gaps	12;

[illegible]

RESULT 14
US-08-184-422-8
Sequence 8, Application US/08184422
Patent No. 556321

GENERAL INFORMATION:

APPLICANT: ARMITAGE, RICHARD
APPLICANT: ARMSTRONG, BARRY
APPLICANT: FANSHAW, WILLIAM
APPLICANT: RENSHAW, BLAIR
APPLICANT: SPRIGGS, MELANIE
APPLICANT: WIDMER, MICHAEL

TITLE OF INVENTION: DETECTION AND TREATMENT OF MUTATIONS
TITLE OF INVENTION: IN A CD40 LIGAND GENE
NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET
CITY: SEATTLE
STATE: WASHINGTON
COUNTRY: USA
ZIP: 98101

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple Operating System 7.1
SOFTWARE: MS Word for Apple 5.1, Version a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/184,422
FILING DATE: *

CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/009,258
FILING DATE: 01/22/93

ATTORNEY/AGENT INFORMATION:
NAME: PERKINS, PATRICIA ANNE
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2810-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 2065870430
TELEFAX: 2065870606

INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 261 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-184-422-8

Query Match 11.5%; Score 150; DB 1; Length 261;
Best Local Similarity 25.4%; Pred. No. 6.8e-09;
Matches 58; Conservative 43; Mismatches 95; Indels 32; Gaps 12;

QY 22 LHEADFDOT--TLESQDTKLIPDSCRRKQAFQAVQKELQHVGSQHIAEKAMVDGS 79
DB 59 LHEDVFEMKTIQRCNTGERSLSLNCCEIKSQEGFV-KDIM-----LNKEETKENS 110
QY 80 WIDLAKRSKLEAOPFAHITNATDIPSGSHKVSLSWYHDGMAKISN--MTFSNGK-LI 136
DB 111 F-EMQKGDQ-NPQIAHAVISEAS-----SKTTSVLQW-AEKGYTMSNNLVTLENGKQLT 162
QY 137 VNODGFYLYIANICFRHHETSGDLATEYLQIMVYVTKTSIKIPS--SHTLMKGSTKYWS 194
DB 163 VKRQGLYIYIAQVTFCSNREASSQAP-----FIASLCLSPGFRERILLRANTH--S 213
QY 195 GNSSEHFYSINVGFFKLRSGEISIEVSNPSLDDPDQATYFGAKV 242
DB 214 SAKPCGQOSIHGQVFEIQPGASVFNVTDPQSVSHGTGFTSFGLKL 261

RESULT 15
US-08-360-923A-2
Sequence 2, Application US/08360923A

Patent No. 5674492

GENERAL INFORMATION:

APPLICANT: ARMITAGE, RICHARD

APPLICANT: FANSLAW, WILLIAM

APPLICANT: LONGO, DAN L.

APPLICANT: MORPHY, WILLIAM

TITLE OF INVENTION: METHOD OF PREVENTING OR TREATING

TITLE OF INVENTION: DISEASE CHARACTERIZED BY NEOPLASTIC CELLS

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: IMMUNEX CORPORATION

STREET: 51 UNIVERSITY STREET

CITY: SEATTLE

STATE: WASHINGTON

COUNTRY: USA

ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

OPERATING SYSTEM: Apple Macintosh System 7.1

SOFTWARE: Microsoft Word for Macintosh, Version #5.1a

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/360,923A

FILING DATE: December 21, 1994

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: USSN 08/172,664

FILING DATE: December 23, 1993

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Perkins, Patricia A.

REGISTRATION NUMBER: 34,693

REFERENCE/DOCKET NUMBER: 2818-A

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206)587-0430

TELEFAX: (206)233-0644

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 261 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-360-923A-2

Query Match 11.5%; Score 150; DB 1; Length 261;
Best Local Similarity 25.4%; Pred. No. 6.8e-09;
Matches 58; Conservative 43; Mismatches 95; Indels 32; Gaps 12;

QY 22 LHEADFDOT--TLESQDTKLIPDSCRRKQAFQAVQKELQHVGSQHIAEKAMVDGS 79
DB 59 LHEDVFEMKTIQRCNTGERSLSLNCCEIKSQEGFV-KDIM-----LNKEETKENS 110
QY 80 WIDLAKRSKLEAOPFAHITNATDIPSGSHKVSLSWYHDGMAKISN--MTFSNGK-LI 136
DB 111 F-EMQKGDQ-NPQIAHAVISEAS-----SKTTSVLQW-AEKGYTMSNNLVTLENGKQLT 162
QY 137 VNODGFYLYIANICFRHHETSGDLATEYLQIMVYVTKTSIKIPS--SHTLMKGSTKYWS 194
DB 163 VKRQGLYIYIAQVTFCSNREASSQAP-----FIASLCLSPGFRERILLRANTH--S 213
QY 195 GNSSEHFYSINVGFFKLRSGEISIEVSNPSLDDPDQATYFGAKV 242
DB 214 SAKPCGQOSIHGQVFEIQPGASVFNVTDPQSVSHGTGFTSFGLKL 261

Search completed: November 1, 2000, 17:58:49
Job time: 10979 sec

Thu Nov 2 16:03:24 2000

us-09-202-455-17.ra1

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